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US-09-513-999C-3894
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Sequence 26253, A
Sequence 10788, A
Sequence 120325,
Sequence 15086, A
Sequence 13658, A
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                                                                                                                                               June 24, 2005, 04:39:48; Search time 129 Seconds (without alignments) 4147.771 Million cell updates/sec
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(cgn2_6/ptodata//ina/5A_COMB.seq:*

(cgn2_6/ptodata/1/ina/5B_COMB.seq:*

(cgn2_6/ptodata/1/ina/6B_COMB.seq:*

(cgn2_6/ptodata/1/ina/6B_COMB.seq:*

(cgn2_6/ptodata/1/ina/6B_COMB.seq:*

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Compugen Ltd
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US-09-949-016-4940

US-09-780-016-27

US-09-513-999C-10371

US-09-621-976-15180

US-09-621-976-15180

US-09-621-976-15180

US-09-270-767-26812

US-09-248-796A-5495

US-09-313-294A-492

US-09-313-294A-492

US-09-949-016-17521

US-09-949-016-17521

US-09-949-016-17521

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US-09-949-016-13658
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  GenCore version
Copyright (c) 1993 - 2005
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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Sequence 3894, Application US/09513999C

Patent No. 6783961

GENERAL INFORMATION:

APPLICANT: Duclert, A.

APPLICANT: Glordano, J.Y.

TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.

PILE REFERENCE: 59.US2.REG

CURRENT APPLICATION NUMBER: US/09/513,999C

CURRENT FILING DATE: 2000-02-24

PRIOR APPLICATION NUMBER: US 60/122,487

PRIOR FILING DATE: 1999-02-26

NUMBER OF SEQ ID NOS: 36681

SOFTWARE: Patent.pm

SEQ ID NO 3894
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                                          1945, Ap
1854, Ap
12706, A
16070, A
5505, Ap
28, Appl
4142, Ap
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12292, A
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3245, Ap
7, Appli
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17127, A
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100.0%; Pred. No. 1.9e-107;
iive 0; Mismatches 0;
US-09-621-976-1817
US-09-599-360B-27
US-09-621-976-1854
US-09-621-976-1854
US-09-949-016-12706
US-09-949-016-12706
US-09-248-796A-5505
US-09-270-767-1942
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US-09-270-767-1942
US-09-248-7058-13-6817
US-09-489-016-12292
US-09-489-016-12292
US-09-489-016-1232
US-09-489-016-12292
US-09-489-016-12292
US-09-489-016-12292
US-09-6343-6817
US-09-643-6817
US-09-643-6817
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Best Local Similarity 100.
Matches 327; Conservative
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PGGANISM: Homo sapiens

FEATURE:
NAME/KEY: CDS

LOCATION: 29..352

FEATURE:
NAME/KEY: misc_feature
LOCATION: 401

OTHER INFORMATION: r=a OF

FEATURE:
NAME/KEY: misc_feature

OTHER INFORMATION: r=a OF

FEATURE:
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US-09-513-999C-3894
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Query Match
Best Local Similarity 98.5%;
Matches 256; Conservative (
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ORGANISM: homo sapiens
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APPLICANT: VENTER, J. Craig et al.

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT PILING DATE: 2000-04-11,

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-09-08

PRIOR PILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 4940
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209 GCGTCCGCTACTTCAGAAGAGTGTACTGTCGCATGGGGAGTCTGTAACCATGCTTTTCAC 268
                                                                  241 ITCCACTGCATCTCCCCTGGCTCAAAACACGACAGGTGTGTCCATTGGACAACAGAGAG 300
                                                                                          61 CGCTTTGAAGTGAAAAAGTGGAATGCAGTAGCCCTCTGGGCCTGGGATATTGTGTGTTGTT 120
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100.0%; Pred. No. 1.9e-107;
ive 0; Mismatches 0;
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Best Local Similarity 100.
Matches 327; Conservative
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ORGANISM: Human
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US-09-949-016-4940
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US-09-780-016-27
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APPLICANT: Donoho, Gregory

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Pred. No. 1.7e-80;
0; Mismatches 4; Indels 0;
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APPLICANT: Scoville, John
APPLICANT: Turner, C. Alexander Jr.
APPLICANT: Abuin, Alejandro
APPLICANT: Zambrowicz, Brian
APPLICANT: Sands, Arthur T.
TITLE OF INVENTION: No. 6743621el Human Proteases and
TITLE OF INVENTION: Polynucleotides Encoding the Same;
TITLE OF INVENTION: Polynucleotides Encoding the Same;
TITLE OF INVENTION: No. 6743621el Human Proteases and
TITLE OF INVENTION: Polynucleotides Encoding the Same;
FILE REPRENCE: L032-013-0-08-07
FRICA PLLING DATE: 2002-08-07
FRICA PLLING DATE: 2001-02-09
FRICA FILING DATE: 2000-02-11
NUMBER OF SEQ ID NOS: 27
SOFTWARE: FRASESEQ for Windows Version 4.0
SEQ ID NO 27
LENGTH: 3208
LENGTH: 3208
LENGTH: ALLOR PLLING DATE: DATE
LENGTH: ALLOR PLLING DATE: NOS: 27
LENGT
APPLICANT: TUTHER, C. Alexander Jr.
APPLICANT: TUTHER, C. Alexander Jr.
APPLICANT: Friedrich, Glenn
APPLICANT: Abuin, Alejandro
APPLICANT: Zambrowicz, Brian
APPLICANT: Zambrowicz, Brian
APPLICANT: Sambrowicz, Brian
TITLE OF INVENTION: No. 6509456el Human Proteases and
TITLE OF INVENTION: No. 6509456el Human Proteases and
TITLE OF INVENTION: No. 6509456el Human Proteases and
TITLE OF INVENTION: No. 6509466l Human Proteases and
TITLE OF INVENTION: NO. 6509466l Human Proteases and
FILE REFERENCE: LEX-013-USA
CURRENT APPLICATION NUMBER: US/09/780,016
CURRENT FILING DATE: 2000-02-11
NUMBER OF SEQ ID NOS: 27
SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 27
LENTH: 3208
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Patent No. 6743621
GENERAL INFORMATION:
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161 GAGICIGIAACCAIGCTITICACTICCACIGCAICTCICGCIGGCICAAAACACGACAGG 220
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                                                   226 TCTGTCCATTGGACAACAGAGAGTGGGAATTCCAAAAGTATGGGCACTAG 275
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                        278 TGTGTCCATTGGACAACAGAGTGGGAATTCCAAAAGTATGGGCCACTAG 327
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Patent No. 6833446
GENERAL INDRAMION:
APPLICANT: Shenk, Marion
APPLICANT: Shenk, Michael A.
APPLICANT: McGrath, Annette
APPLICANT: Glenn, Matthew
TITLE OF INVENTION: Compositions and Methods for the
TITLE OF INVENTION: Modification of Gene Transcription
TILLE REFERENCE: 11000.1021C1U
CURRENT APPLICATION NUMBER: US/09/640,211A
CURRENT FILLS CONTRACT APPLICATION NUMBER: US/09/640,211A
CURRENT FILLS OF SEQ ID NOS: 2368
SOFTWARE: PastSEQ for Windows Version 4.0
                                                                                                                                               RESULT 6
US-09-621-976-15180

; Sequence 15180, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Johnas Milne Edwards, J.B.
; APPLICANT: Glordano, J.Y.
; TITLE OF INVENTION: ESTS and Encoded Human Proteins.
; FILE REPERENCE: GENERIC 1054 PR2.
; CURRENT APPLICATION UNMER: US/09/621,976
; CURRENT PILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 15180
; LENGTH: 463
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc_feature

LOCATION: 74

// OTHER INFORMATION: n=a, g, c or t

US-09-621-976-15180
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Matches 170; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                   2885 CTACTTCAGAAGAGIGIACIGICGCAIGGGGAGICIGIAACCAIGCTTTTCACTTCCACT 2944
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; Sequence 10311, Application US/09513999C
; Patent No. 6783961;
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.;
; APPLICANT: Glordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; PILE REFERENCE: 59, USZ. REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT PILING DATE: 2000-02-24
; PRIOR PILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SEQ ID NO 10371
LENGTH: 402
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                                                                                                                                                       68 AAGTGAAAAAGTGGAATGCAGTAGCCCTCTGGGCCTGGGATATTGTGGTTGATAACTGTG 127
                                                                                                                                                                                                                                                              128 CCATCTGCAGGAACCACATTATGGATCTTTGCATAGAATGTCAAGCTAACCAGGCGTCCG 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      248 GCATCTCTCGCTGGCTCAAAACACGACAGGTGTGTCCATTGGACAACAGAGAGTGGGAAT 307
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                                                Query Match 77.6%; Score 253.6; DB 4; Length 3208; Best Local Similarity 98.5%; Pred. No. 1.7e-80; Matches 256; Conservative 0; Mismatches 4; Indels 0;
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Matches 170; Conservative
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NAME/KEY: misc_feature
LOCATION: 20
OTHER INFORMATION: k=g
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NAME/KEY: misc_feature
LOCATION: 38
OTHER INFORMATION: s=g
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NAME/KEY: misc_feature
LOCATION: 79
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ORGANISM: Homo sapiens
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US-10-214-811-27
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239 ACTICCACTGCATCTCTCGCTGGCTCAAAACACGGCGGGGTGTGTCCATTGGACAAGAGG
                                                                                                  ; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-11265
                                                                                                                                                                              42.3%;
nilarity 71.0%;
Conservative 0,
CURRENT FILING DATE: 1999-03-17
                NUMBER OF SEQ ID NOS: 62517
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 11265
LENGTH: 1101
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Best Local Similarity 66.8
Matches 179; Conservative
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nes 198; Conserv
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US-09-248-796A-5495
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CAAGCTAACCAGGCGTCCGCTACTTCAGAAGAGTGTACTGTCGCATGGGGAGTCTGTAAC 228
                                                                                                    161 AAACGTTTCGAAATCAAGAAGTGGAATGCTGTAGCCCTTTGGGGGGTGTTGTGGGTT 220
                                                                                                                                                               118 GATAACTGTGCCATCTGCAGGAACCACTTATGGATCTTTGCATAGAATGTCAAGCTAAC 177
                                                                                                                                                                                      221 GATAATTGTGCAATTTGCAGAAACCACATCATGGACCTCTGTGTATTGAGTGTCAGGCAAAT 280
                                                                                                                                                                                                                                               CAGGCGTCCGCTACTTCAGAAGAGTGTACTGTCGCATGGGGAGTCTGTAACCATGCTTTT 237
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Patent No. 6703491
GENERAL INFORMATION
GENERAL INFORMATION
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT APPLICATION NUMBER: US/09/270,767
SUMPRENT PATELNG DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62217
SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Homburger et al. TITLE OF INVENTION: Nocleic acids and proteins of Drosophila melanogaster FILE REFERENCE: File Reference: 7326-094 CURRENT APPLICATION NUMBER: US/09/270,767
                                                                                                                                                                                                                                                                                                                             238 CACTICCACIGCATCICTCGCIGGCICAAAACACGACAGGIGIGICCATIGGACAACA 295
                                                                                                                                                                                                                                                                                                                                                    341 CATTICCATIGCATAAGICGGTGGCTCAAGACACGACAAGICTGCCCATIAGATAATA 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            109 ATTGTGGTTGATAACTGTGCCATCTGCAGGAACCACATTATGGATCTTTGCATAGAATGT
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Length 411;
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                                       53; Indels
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Score 153.2; DB 4;
Pred. No. 8.4e-45;
0; Mismatches 53;
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US-09-270-767-11265/c
Sequence 11265, Application US/09270767
Patent No. 6703491
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA ORGANISM: Drosophila melanogaster
Query Match
Best Local Similarity 77.7%;
Matches 185; Conservative
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US-09-270-767-26812/c
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LENGTH: 490
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Sequence 5495, Application US/09248796A

Sequence 5495, Application US/09248796A

Sequence 5495, Application US/09248796A

Patent No. 674137

GENERAL INFORMATION:

TITLE OF INVENTION: WUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANK;

TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS

CURRENT APPLICATION NUMBER: US 60/074,725

PRIOR APPLICATION NUMBER: US 60/074,725

PRIOR FILING DATE: 1998-02-13

PRIOR FILING DATE: 1998-08-13

NUMBER OF SEQ ID NOS: 28208

SEQ ID NOS: 28208
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                                                                                                                                                                              933 GCCAGGACGGAGCGCTTTGTGGTGAAAAAGGGTTGCGCACGCCATGTGGGATGGGAC 874
                                                                                                                                                                                                                                                                                                                                                                                                   CAAGCTAACCAGGCGTCCGCTACTTCAGAAGAGTGTACTGTCGCATGGGGAGTCTGTAAC 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     757
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             109 ATTGTGGTTGATAACTGTGCCATCTGCAGGAACCACATTATGGATCTTTGCATAGAATGT 168
                                                                                                                                                                                                                                                                                                                                    873 GTAĞCAĞTGGACAACTGTGCCATCTGCCGTAACCACATCATGAACCTGTGCATCGAGTGC 814
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            209 IGGGIAATATICCTICAGAAGAGIGIATICCIGCTIGGGGAGIAIGIAATCAIGCATITIC
                                                                                                                                    49 GCGGCCAAGAAGCGCTTTGAAGTGAAAAGTGGAATGCAGTAGCCCTCTGGGCCTGGGAT
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                                                                  3,
   Length 1101;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        289 GACAACAGAGAGTGGGAATTCCAAAAGTATGGGCACTAG 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  696 GACAACAAGGAGTGGTCTACCAGAAGTACGGCCGCTAG 658
Score 138.2; DB 4;
Pred. No. 3.9e-39;
0; Mismatches 78;
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38 CCAACAGCGGCGCGGCAAGAAGCGCTTTGAAGTGAAAAAGTGGAATGCAGTAGCCCTCT
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APPLICANT: Issakani, Sarkiz D.
APPLICANT: Huang, Jianing
APPLICANT: Sheung, Julie
APPLICANT: Rangel Pharmaceuticals, Inc.
APPLICANT: Rigel Pharmaceuticals, Inc.
APPLICANT: Rigel Pharmaceuticals, Inc.
TILLE OF INVENTION: Ubiquitin Ligase Assay
FILE REFERENCE: 021044-007010US
CURRENT APPLICATION NUMBER: US/09/826,312A
CURRENT FILING DATE: 2001-04-03
PRIOR FILING DATE: 2000-04-03
NUMBER: OF SEQ ID NOS: 21
SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; FEATURE:
; OTHER INFORMATION: RING finger protein ROC2
US-09-826-312A-7
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Patent No. 6740495
GENERAL INFORMATION:
APPLICANT: ISBERANI, Sarkiz D.
APPLICANT: Huang, Jianing
APPLICANT: Shueng, Jilie
TITLE OF INVENTION: UBIQUITIN LIGASE ASSAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            292 AACAGAGAGTGGGAATTCCAAA 313
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                                                                                                                                                                                                                                                                                                                              ; Sequence 7, Application US/09826312A; Patent No. 6737244
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US-09-826-312A-7
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US-09-542-497A-7
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Patent No. 681239

GENERAL INFORMATION:
APPLICANT: VENTER,
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
TITLE REFERENCE: CL001307
CURRENT FILING DATE: 2000-04-14
FRIOR APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/231,768
PRIOR PILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
NUMBER OF SEQ ID NOS: 207012
SEQ ID NO 16628
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Patent No. 647632
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Lalgudi, Raghunath V.
APPLICANT: Ito, Laura Y.
APPLICANT: Sherman, Bradley K.
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN BAR FILE REFERENCE: P-0017 US
CURRENT APPLICATION NUMBER: US/09/313,294A
CURRENT FILING DATE: 1999-05-14
NUMBER OF SEQ ID NOS: 7600
SOFTWARE: PERL PROGRAM
SEQ ID NO 492
LENGTH: 301
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27.5%; Score 90; DB 4; Length 301; 74.0%; Pred. No. 4.4e-22; tive 0; Mismatches 40; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18463 GTCCATTGGACAACAGAGAGTGGGAATTCCAAAAGTAGG 18501
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; OTHER INFORMATION: Incyte ID No. 6476212 700549333H1
US-09-313-294A-492
                                                                    299 AGTGGGAATTCCAAAAGTATGGGCACTA 326
                                                                                                          329 ATTGGACTTATCAAAATTGGGTAATTA 356
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Best Local Similarity 74.0
Matches 114; Conservative
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Best Local Similarity
Matches 95; Conserv
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ORGANISM: Zea mays
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US-09-313-294A-492
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146 cercercecedaagecedaagageerregagareaagagagagagagagageerer 205
                                                                          GGGCCTGGGATATTGTGTGGTTGATAACTGTGCCATCTGCAGGAACCACATTATGGATCTTT 157
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                                                                                                                                                                                                                   158 GCATAGAATGTCAAGCTAACCAGGCGTCCGCTAC 191
                                                                                                                                                                                                                                                                                   266 gcarcaagraccagaagaaagaagaagaaga 299
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US-09-799-451-296

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Search completed: June 24, 2005, 06:37:49 Job time : 232 secs
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                                                                                                                                                                                                                                                                                                        52 GCCAAGAAGCGCTTTGAAGTGAAAAGTGGAATGCAGTAGCCCTCTGGGCCTGGGATATT 111
                                                                                                                                                                                                                                                                                                                                                                                                             172 GCTAACCAGGCGTCCGCTACTTCAGAAGAGTGTACTGTCGCATGGGGAGTCTGTAACCAT 231
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    232 GCTTTTCACTTCCACTGCATCTCTCGCTGGCTCAAAACACGACGAGGTGTGTCCATTGGAC 291
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                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                          Length 342;
                                                                                                                                                                                                                        Score 74; DB 4; Length 342
Pred. No. 2.8e-16;
0; Mismatches 100; Indels
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TITLE OF INVENTION: No. 6783969e1 Nucleic Acids and
TITLE OF INVENTION: No. 6783969e1 Nucleic Acids and
TITLE OF INVENTION: Polypeptides
FILE REPERBNCE: 803
CURRENT APPLICATION NUMBER: US/09/799,451
CURRENT FILING DATE: 2001-03-05
NUMBER OF SEC ID NOS: 948
SOFTWARE: DL_Genes Version 2.0
SEQ ID NO 296
FILE REFERENCE: A-68613/RMS/JJD
CURRENT APPLICATION NUMBER: US/09/542,497A
CURRENT FILING DATE: 2000-04-03
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patentin version 3.1
SEQ ID NO 7
LENGTH: 342
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Patent No. 6783969
GENERAL INFORMATION:
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Zhao, Qing A.
Wang, Jian-Rui
Ma, Yunqing
Yamazaki, Victoria
Chen, Rui-hong
                                                                                                                                                                                                                          Query Match
22.6%;
Best Local Similarity 58.4%;
Matches 153; Conservative
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APPLICANT: Zhou, Ping
APPLICANT: Goodrich, Ryle
APPLICANT: Asundi, Vinod
APPLICANT: Ren, Feiyan
APPLICANT: Ren, Feiyan
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Wehrman, Tom
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Ghosh, Reena
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                             TYPE: DNA
ORGANISM: Homo sapiens
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LOCATION: (81)..(431)
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US-09-799-451-296
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APPLICANT:
APPLICANT:
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APPLICANT:
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130 cceselacrcasscrccaasrcssaasescacaasatsrrcrccrcaasaastsaass
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                                                                                                                                                                                                         190 CGGTGGCCATGTGGAGCTGGAGCGTGCGATACGTGCGCCATCTGCAGGTCCAGG 249
                                                                                          26 CCCCGAGCGGCCCCAACAGCGGCGCGGCCAAGAGCGCTTTGAAGTGAAAAAGTGGAATG
                                                  Gaps
                                               ö;
  Length 439;
Query Match
14.2%; Score 46.4; DB 4; Length 4
Best Local Similarity 60.2%; Pred. No. 2.9e-06;
Matches 77; Conservative 0; Mismatches 51; Indels
                                                                                                                                                                                                                                                                                146 TTATGGAT 153
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96, App 6253, A 67, App

304, App 4980, App 2, Appli 1, Appli 763, App 11319, App 1319, App 2214, App 220, App

3134, Ap 11, Appl 1, Appli 7, Appli

16245,

Perfect score:

Sequence:

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Scoring table:

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Length:
                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 3894, Application US/09513999C
; Patent No. 6783961
; GENERAL INDEMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1.7e-69
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  TYPE: DNA
ORGANISM: Homo sapiens
FRATURE:
NAME/KEY: CDS
LOCATION: 29..352
FRATURE:
NAME/KEY: misc_feature
LOCATION: 401
OTHER INFORMATION: r=a or
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US-09-513-999C-3894
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc feature
   US-09-513-999C-3894
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   Command line parameters:
-MODBL=frame+ p2n.model-UBV=xlh
-Q=/Cgn2_1/USPTO_spool/US09541462/runat_23062005_122624_9498/app_query.fasta_1.263
-Q=/Cgn2_1/USPTO_spool/US09541462/runat_23062005_122624_9498/app_query.fasta_1.263
-Q=/Cgn2_1/USPTO_spool/US09541462_runat_BINEARIN_=IMATRIX=blosum62_-TRANS=human40.cdi
-LOOPEXT=0 -UNITS=Dits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR SCORES=pct -THR MAX=100 -THR MINEO -ALIGN=155
-USFR=US09541462_@CGN 1 1_69_@runat_23062005_122624_9498_-NCPU=6 -ICPU=3
-NOMBL-LOCAL -OUTFMT=pto -NORM=ext -HEAPSTEIZE=500 -MINLEN=0 -MAXLEN=200000000
-USFR=US09541462_@CGN 1 1_69_@runat_23062005_122624_9498_-NCPU=6 -ICPU=3
-NOM ANAP -LARGEQUERY -NGG SCORES=0 -MAIT -DSPBLOCK=100 -LONGIAG
-PRAPEXT=1 -YGAPOP=10 -YGAPEXT=0.5 -PGAPOP=6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 27, Appl
Sequence 27, Appl
Sequence 1731, Ap
Sequence 16812, A
Sequence 11265, A
Sequence 10371, A
Sequence 5495, Ap
Sequence 7, Appli
Sequence 7, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 3894, Ap
Sequence 4940, Ap
                                                                   June 24, 2005, 08:28:03; Search time 156 Seconds (without alignments) 1132.807 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                      616
1 MAAAMDVDTPSGTNSGAGKK......KTRQVCPLDNREWEFQKYGH 108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       /cgn2_6/ptodata/1/ina/SA_COMB.seq:*
/cgn2_6/ptodata/1/ina/SB_COMB.seq:*
/cgn2_6/ptodata/1/ina/6A_COMB.seq:*
/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
/cgn2_6/ptodata/1/ina/PcTUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/PcTUS_COMB.seq:*
           GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd
                                                  - nucleic search, using frame_plus_p2n model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-513-999C-3894
US-09-949-016-4940
US-09-780-016-27
US-10-214-811-27
US-09-640-211A-1731
US-09-270-767-26812
US-09-513-999C-10371
US-09-513-999C-10371
US-09-621-976-15180
US-09-248-796-5495
US-09-826-312A-7
US-09-542-497A-7
                                                                                                                                                                                                                                Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                             1202784 segs, 818138359 residues
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                                                                                                                                                                                                                                                                                 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                             Xgapop 10.0 , Xgapext
Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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Maximum DB seq length: 200000000
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Match Length DB
                                                                                                                                                   BLOSUM62
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Score 616 616

Result

Database :

501.5 501.5 479 400.5

394 394 375.5 287 287

2

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56 CysGlnAlaAsnGlnAlaSerAlaThrSerGluGluCysThrValAlaTrpGlyValCys 75
67 CGCTTTGAAGTGAAAAAGTGGAATGCAGTAGCCCTCTGGGCCTGGGATATTGTGTGTTGAT 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  76 AsnHisAlaPheHisPheHisCysIleSerArgTrpLeuLysThrArgGlnValCysPro 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2752 GGAGCATAAAAAAAAAAAA------AAAAAATGGAATGGGGCTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16 GlyAlaGlyLysLysLysArgPheGluValLysLysTrpAsnAlaValAlaLeuTrpAlaTrp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL NO. 95049420.
GENERAL THORMATTON:
APPLICANT: Donoho, Gregory
APPLICANT: Scoville, John
APPLICANT: Tricer, C. Alexander Jr.
APPLICANT: Tricer, C. Alexander
APPLICANT: Abuin, Alejandro
APPLICANT: Sands, Arthur T.
TITLE OF INVENTION: No. 6509456el Human Proteases and
TITLE OF INVENTION: No. 6509456el Human Proteases and
TITLE OF INVENTION: No. 6509456el Human Proteases and
TITLE OF INVENTION: No. 6509456el Human Proteases
CURRENT FILING DATE: 2001-02-09
PRIOR PLLING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: US 60/181,294
PRIOR PLLING DATE: 2000-02-11
NUMBER OF SEQ ID NOS: 27
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3208
88
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3
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Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                  TrpGluPheGlnLysTyrGlyHis 108
                                                                                                                                                                                                                                                                                      Sequence 27, Application US/09780016
Patent No. 6509456
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95.70%
94.62%
81.41%
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CORGANISM: homo sapiens
US-09-780-016-27
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Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Alignment Scores:
Pred. No.:
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LENGTH: 3208
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; Sequence 4940. Application US/09949016
; Patcent No. 681239
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF; FILE REFERENCE: CLOOU3307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR PILING DATE: 2000-10-20
; PRIOR FILING DATE: 2000-10-03
; PRIOR FILING DATE: 2000-10-03
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTHARE: FeatSEQ for Windows Version 4.0
; SEQ ID NO 4940
                                                                                                                                                                                                                                                                                                                                               PheHisCysIleSerArgTrpLeuLysThrArgGlnValCysProLeuAspAsnArgGlu 100
                                                                                                                                                                                       149 AACTGTGCCATCTGCAGGAACCACATTATGGATGCTTGCATAGAATGTCAAGCTAACCAG 208
                                                                                                                                                                                                                                                                                                          209 GCGTCCGCTACTTCAGAAGAGTGTACTGTCGCATGGGGAGTCTGTAAACCATGCTTTTCAC 268
                                                                                                                                                                                                                                                                                                                                                                 21 ArgPheGluValLysLysTrpAsnAlaValAlaLeuTrpAlaTrpAspIleValValAsp 40
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                                                                                                                                 29 ATGGCGGCAGCGATGGATGTGGATACCCCGAGCGGCACCAACAACAGCGGCGCGGGCAAGAAG 88
                                                                                                                                                                        21 ArgPheGluValLysLysTrpAsnAlaValAlaLeuTrpAlaTrpAspIleValValAsp 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 AlaSerAlaThrSerGluGluCyBThrValAlaTrpGlyValCysAsnHisAlaPheHis
                                                                                                                  1 MetalaalaalametaspValaspThrProSerGlyThrAsnSerGlyAlaGlyLysLys
108
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1108
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                                                                                      US-09-541-462B-2 (1-108) x US-09-513-999C-3894 (1-482)
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Matches:
Conservative:
Mismatches:
              Conservative:
Mismatches:
Indels:
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  Matches:
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              Percent Similarity:
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Best Local Similarity:
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ORGANISM: Human
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US-09-949-016-4940
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CURRENT APPLICATION NUMBER: US/09/640,211A
CURRENT FILING DATE: 2000-08-16
NUMBER OF SEQ ID NOS: 2368
SOFTWARE: PSELSEQ for Windows Version 4.0
LENGTH: 411
                                                                                                                                                                                             ; LOCATION: (1)...(411)
; OTHER INFORMATION: n = A,T,C or
US-09-640-211A-1731
                                                                                                                                                                                                                                                                              4.28e-52
479.00
84.96%
79.65%
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400.50
77.57%
65.42%
65.02%
                                                                                                                   TYPE: DNA ORGANISM: Pinus radiata
                                                                                                                                                                         NAME/KEY: misc feature
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Best Local Similarity:
Query Match:
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2803 GATATTGFGGTTGATAACTGTGCCATCTGCAGGAACCACATTATGGATCTTTGCATAGAA 2862
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              56 CysGlnAlaAsnGlnAlaSerAlaThrSerGluGluCysThrValAlaTrpGlyValCys 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16 GlyAlaGlyLysLysArgPheGluValLysLysTrpAsnAlaValAlaLeuTrpAlaTrp 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   36 AspileValValAspAsnCysAlaIleCysArgAsnHisIleMetAspLeuCysIleGlu 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2863 TGTCAAGCTAACCAGGCGTCCGCTACTTCAGAAGAGTGTACTGTCGCATGGGGAGTCTGT
                                                                                                                               APPLICANT: Donolo, Gregory
APPLICANT: Scoville, John
APPLICANT: Turner, C. Abrander Jr.
APPLICANT: Turner, C. Abrander Jr.
APPLICANT: Abuin, Alejandro
APPLICANT: Zambrowicz, Brian
APPLICANT: Zambrowicz, Brian
APPLICANT: Sands, Arthur T.
TILLE OF INVENTION: No. 6743621el Human Proteases and
TITLE OF INVENTION: No. 6743621el Human Proteases and
TITLE OF INVENTION: No. 6743621el Human Proteases and
TITLE OF INVENTION: No. 6743621el Human Proteases
FILE REPERENCE: LESS 0132016
FRIOR FILING DATE: 2002-08-07
PRIOR FILING DATE: 2001-02-09
PRIOR FILING DATE: 2000-02-11
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Patent No. 6833446
GENERAL INFORMATION:
APPLICANT: Wood, Marion
APPLICANT: Mood, Michael A.
APPLICANT: McGrath, Annette
APPLICANT: Glenn, Matthew
TITLE OF INVENTION: Compositions and Methods for the
TITLE OF INVENTION: Modification of Gene Transcription
FILE REFERENCE: 11000.1021C1U
  2983 TTGGACAACAGAGAGTGGGAATTCCAAAAGTATGGGCAC 3021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2983 ricgacaacadadagicgdaariccaaaagrarcgccac 3021
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 27
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                          ; Sequence 27, Application US/10214811; Patent No. 6743621
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501.50
95.70%
94.62%
81.41%
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US-10-214-811-27
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Query Match:
DB:
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US-09-640-211A-1731
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LENGTH: 3208
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254 GACCTCTGTATTGAGTGTCAGGCAAATCAAGCAAGTGCAACAAGTGAAGAATGTACTGTT 313
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Sequence 2012, Application US/09270767

Sequence 8012, Application US/09270767

GENERAL INFORMATION:

APPLICANT: Homburger et al.

TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster.

FILE REFERENCE: File Reference: 7326-094

CURRENT APPLICATION NUMBER: US/09/270,767

CURRENT PILING DATE: 1999-03-17

NUMBER OF SEQ ID NOS: 62517

SOFTWARE: PATENTIN Ver. 2.0

SEQ ID NO 26812

LENGTH: 490
                                                                                                                                                                                                                                                                                                         71 AlaTrpGlyValCysAsnHisAlaPheHisPheHisCysIleSerArgTrpLeuLysThr
                                                                                                                                                                                                                                                                                     3 AlaAlaMetAspValAsp-----ThrProSer-----GlyThrAsnSerGlyAla
                                                                                                                                                                                                                                                                                                                                                                         -----LystysArgPheGluValLystysTrpAsnAlaVal
                                                                                                                                                                                                                                                                                                                                                                                                               134 GGACCAAGCGCTTCCACCAAGAAGGCCAAACGTTTCGAAATCAAGAAGTGGAATGCTGTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                             31 AlaLeuTrpAlaTrpAspIleValValAspAsnCysAlaIleCysArgAsnHisIleMet
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Matches:
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Mismatches:
Indels:
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; ORGANISM: Drosophila melanogaster
US-09-270-767-26812
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| FENCINA NO. 0.03.04. |
| GENERAL INFORMATION: |
| APPLICANT: Duclert, A. |
| APPLICANT: Giordano, J.Y. |
| TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins. |
| PALEN NO. 6783961 |
| FILE REFERENCE: 5.9.US2.REG |
| FILE REFERENCE: 5.9.US2.REG |
| CURRENT APPLICATION NUMBER: US/09/513,999C |
| CURRENT APPLICATION NUMBER: US 60/122,487 |
| PRIOR PILING DATE: 1999-02-26 |
| NUMBER OF SEQ ID NOS: 36681 |
| SOFTWARE: PETENT NEW SECOLES |
| SOFTWARE: PETENT NEW SECOLES |
| SOFTWARE: PETENT NEW SECOLES |
| LENGTH: 402 |
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744 TACCACTGCATCGCGCGCGCGTGAAAACGCGCCTGGTCTGTCCGCTGGACAACAAGGAG 685
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Patent No. 6783961
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                                                           101 TrpGluPheGlnLysTyrGly 107
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OTHER INFORMATION: k=g
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NAME/KEY: misc_feature
*ACATION: 79
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LOCATION: 20
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Best Local Similarity:
                                                                                                                                                                    RESULT 8
US-09-513-999C-10371
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                                                                                                                                                                                                                                                                                                                                                                                                                                     112 GCGGTAGCGTTTTGGTCATGGGATATGCAAATTGAAAATTGTGCCATTTGTAGAAATCAT 171
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           68 CysThrValAlaTrpGlyValCysAsnHisAlaPheHisPheHisCysIleSerArgTrp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            232 TGTATTCCTGCTTGGGGAGTATGTAATCATGCATTTCATTTACATTGTATTAGAAGATGG
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62
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Matches:
Conservative:
Mismatches:
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Matches:
Conservative:
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APPLICANT: Huang, Jianing
APPLICANT: Huang, Jianing
APPLICANT: Sheung, Julie
APPLICANT: Sheung, Julie
APPLICANT: Pray, Todd R.
APPLICANT: Rigel Pharmaceuticals, Inc.
TITLE OF INVENTION: Ubiquitin Ligase Assay
FILE REFERENCE: 021044-007010US
CURRENT FILING DATE: 2001-04-03
PRIOR APPLICATION NUMBER: US 09/542,497
PRIOR PILING DATE: 2000-04-03
NUMBER OF SEQ ID NOS: 21
SOFTWARE: Patentin Ver. 2.1
SENGTH: 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: RING finger protein ROC2
   60/096,409
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                                                                                                                                                                         5.82e-39
375.50
73.27%
61.39%
PRIOR APPLICATION NUMBER: US 6
PRIOR FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208
SEQ ID NO 5495
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                                                                                                         Candida albicans
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                                                                                       TYPE: DNA ORGANISM: (
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APPLICANT: Keith Weinstock et al

APPLICANT: Keith Weinstock et al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN

TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107196.132

CURRENT APPLICATION NUMBER: US/09/248,796A

CURRENT PILING DATE: 1999-02-12

PRIOR APPLICATION NUMBER: US 60/074,725

PRIOR FILING DATE: 1998-02-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  103 ------ATAGAATGTCAAGCTAAACGGGGGCGTCGCTACT 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       196 TCTCGCTGGCTCAAAACACGACAGGTGTGTCCATTGGACAACAGAGAGTGGGAATTCCAA 255
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LysLysTrpAsnAlaValAlaLeuTrpAlaTrpAspIleValValAspAsnCysAlaIle 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             45 CysArgAsnHisIleMetAspLeuCysIleGluCysGlnAlaAsnGlnAlaSerAlaThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    65 SerGluGluCysThrValAlaTrpGlyValCysAsnHisAlaPheHisPheHisCysIle
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US-09-248-796A-5495
Sequence 5495, Application US/09248796A
; Patent No. 6747137
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256 AAGTATGGGCAC 267
 261 AAGTATGGGCAC 272
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NAME/KEY: misc_feature
LOCATION: 74
                                                                                                                                                                                                                                                                                                                                          ORGANISM: Homo sapiens
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Best Local Similarity:
Query Match:
DB:
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OTHER INFORMATION: Incyte ID No. 6476212 700549333H1
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Mismatches:
Indels:
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Matches:
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; Patent No. 6548633
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                    1.24e-24
262.50
71.43%
66.23%
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Best Local Similarity:
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                                           RESULT 13
US-09-313-294A-492
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                                                                                                      AspleuCyslleGluCysGlnAlaAsnGlnAlaSerAlaThrSerGluGluCysThrVal 70
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                                                                                                                                             31 AlaLeuTrpAlaTrpAspIleValValAspAsnCysAlaIleCysArgAsnHisIleMet
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                                                          US-09-541-462B-2 (1-108) x US-09-826-312A-7 (1-342)
                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Issakani, Sarkiz D.
APPLICANT: Huang, Jianing
APPLICANT: Huang, Jianing
TITLE OF INVENTION: UBIQUITIN LIGASE ASSAY
FILE REFERENCE: A-68613/RMS/JJD
CURRENT APPLICATION NUMBER: US/09/542,497A
CURRENT FILING DATE: 2000-04-03
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                          RESULT 12
US-09-542-497A-7
Sequence 7, Application US/09542497A
Patent No. 6740495
GENERAL INFORMATION:
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287.00
63.92%
49.48%
46.59%
  49.48%
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US-09-542-497A-7
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JAPPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Bougueleret, L.
APPLICANT: Dobert, S.
TITLE OF INVENTION: Complementary DNA's Encoding Proteins with Signal Peptides
TITLE REFERENCE: GENSET.050CP3
CURRENT APPLICATION NUMBER: 00/13,686
PRIOR PILING DATE: 1998-12-22
PRIOR APPLICATION NUMBER: 60/114,032
PRIOR APPLICATION NUMBER: 60/141,032
PRIOR APPLICATION NUMBER: 09/469,099
PRIOR PLING DATE: 1999-12-21
NUMBER OF SEQ ID NOS: 123
SOFTWARE: Patent.pm
SEQ ID NO 27
Sequence 492, Application US/09313294A

Patent No. 6476212

GENERAL INFORMATION:
APPLICANT: Lalgudi, Raghunath V.
APPLICANT: Lolgudi, Raghunath V.
TITLE OF INVENTION:
POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR
TITLE OF INVENTION:
POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR
CURRENT APPLICATION NUMBER: US/09/313,294A

CURRENT FILING DATE: 1999-05-14
NUMBER OF SEQ ID NOS: 7600
SOFTWARE: PERL PROGram
SEQ ID NO 492
LENGTH: 301
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Von Heijne matrix score 4.4000009536743 seq GILILIPHAGADG/CW

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) OTHER INFORMATION:
) OTHER INFORMATION:
) OTHER INFORMATION:
US-09-621-976-1817
                                                                     Alignment Scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----CysProLeuAspAsnArgGluTrpGluPheGlnLysTyrGly 107
                                                                                                                                                                                                                                                                                                                                                           22 PheGlu------
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APPLICANT: Johert, S.
APPLICANT: Glordano, J.Y.
TITLE OF INVENTION: BSTS and Encoded Human Proteins.
FILE REPERENCE: GENSET. 054PR2
CURRENT APPLICATION UNMBER: US/09/621, 976
CURRENT FILIG DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 1817
LENGTH: 534
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43
18
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                            2.36e-18
217.00
44.53%
31.39%
35.23%
                                                   NAME/KEY: CDS
LOCATION: 187..438
NAME/KEY: polyA signal
LOCATION: 612..617
NAME/KEY: polyA site
              TYPE: DNA
ORGANISM: Homo Sapiens
PEATURE:
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LOCATION: 106..441
NAME/KEY: 8ig_peptide
LOCATION: 106..423
                                                                                                                                                                                           Score:
Percent Similarity:
Best Local Similarity:
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                                                                                                                                                                Alignment Scores:
Pred. No.:
                                                                                                                           , LOCATION: 632
US-09-599-360B-27
  LENGTH: 648
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                                                                                                                                                             35 TrpAspIleValValAspAsnCysAlaIleCysArgAsnHisIleMetAspLeuCysIle
                                                                                                                                            2 AlaAlaAlaMetAspvalAspThrProSerGlyThrAsnSerGlyAlaGlyLysLysArg
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 534
42
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Length:
Matches:
Conservative:
Mismatches:
                                                                                                              US-09-541-462B-2 (1-108) x US-09-621-976-1817 (1-534)
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Job time : 159 secs
   2.3e-16
200.50
51.72%
36.21%
                                                                32.5$
                               Percent Similarity:
Best Local Similarity:
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11029, A 45203, A 9, Appli 15, Appl 57487, A

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TYPE: PRT
ORGANISM: Homo sapiens
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Sequence 7971, Ap
Sequence 1951, Ap
Sequence 1959, A
Sequence 8, Appli
Sequence 77, Appli
Sequence 5, Appli
Sequence 5, Appli
Sequence 577, Appli
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Sequence 578, Appli
Sequence 10851, Ap
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Sequence 2789, Ap
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18, Appl
15483, A
42746, A
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                                                                                                                                                   June 23, 2005, 15:20:31 ; Search time 43 Seconds (without alignments) 187.491 Million cell updates/sec
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                                                                                                                                                                                                                                                                616
1 MAAAMDVDTPSGTNSGAGKK.....KTRQVCPLDNREWEFQKYGH 108
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1: /cgn2_6/ptodata/1/laa/5A_COMB.pep:*
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3: /cgn2_6/ptodata/1/laa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/laa/6B_COMB.pep:*
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6: /cgn2_6/ptodata/1/laa/PCTUS_COMB.pep:*
                    GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-09-949-016-10811
US-09-846-1128-8
US-09-842-4978-8
US-09-542-4978-8
US-09-559-3608-77
US-09-561-3128-5
US-09-621-976-5677
US-09-621-976-5677
US-09-621-976-5714
US-09-949-016-6249
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US-09-949-016-9085
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US-09-270-767-47809
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US-08-933-750C-48
US-09-234-613-48
US-09-949-016-11029
US-09-270-767-45203
US-09-052-089A-15
US-09-270-767-47487
US-09-270-767-42211
US-09-270-767-42211
US-08-63-60A-106
US-08-867-057-3
US-09-128-369-1
US-09-128-369-1
US-09-128-369-3
US-09-949-016-9938
US-09-949-016-9938
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Issakani, Sarkiz D.
APPLICANT: Huang, Jianing
APPLICANT: Huang, Julia
APPLICANT: Pray, Todd R.
TPLE CANT: Rigel Pharmaceuticals, Inc.
TITLE OF INVENTION: Ubiquitin Ligase Assay
FILE REFERENCE: 021044-007010US
CURRENT APPLICATION NUMBER: US/09/826,312A
CURRENT APPLICATION NUMBER: US/09/826,312A
CURRENT APPLICATION NUMBER: US/09/826,497
PRIOR PILING DATE: 2000-04-03
NUMBER OF SEQ ID NOS: 21
SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 6, Application US/09542497A
Patent No. 6740495
GENERAL INFORMATION:
APPLICANT: 168akani, Sarkiz D.
APPLICANT: Huang, Jianing
APPLICANT: Shueng, Julie
TITLE OF INVENTION: UBIQUITIN LIGASE ASSAY
FILLE REPERENCE: A-68613/RMS/JJD
CURRENT APPLICATION NUMBER: US/09/542,497A
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US-09-826-312A-8
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US-09-949-016-10811
i Sequence 10811, Application US/09949016
j Faquence 10811, Application US/09949016
j Patent No. 6812339
j GENERAL INFORMATION:
j APPLICATION: VALUER, J. Craig et al.
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
j FILE REPERRINCE. CL001307
j CURRENT PAPLICATION NUMBER: US/09/949,016
j CURRENT FILING DATE: 2000-04-14
j PRIOR APPLICATION NUMBER: 60/241,755
j PRIOR FILING DATE: 2000-10-03
j PRIOR FILING DATE: 2000-10-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 7971, Application US/09513999C

Batent No. 6783961

GENERAL INPORMATION:

APPLICANT: Duclert, A.

APPLICANT: Duclert, A.

TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.

FILE REFERENCE: 59.105.REG

CURRENT APPLICATION NUMBER: US/09/513,999C

CURRENT APPLICATION NUMBER: US 60/122,487

PRIOR FILING DATE: 2000-02-24

PRIOR FILING DATE: 1999-02-26

NUMBER OF SEQ ID NOS: 36681

SOFTWARE: PATENT. PM.
                                                                                                                                                                                                                                                                                                             1 MAAAMDVDTPSGTNSGAGKKRFEVKKWNAVALWAWDIVVDNCAICRNHIMDLCIECQANQ 60
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                                                                                                                                                                                              100.0%; Score 616; DB 4;
100.0%; Pred. No. 4.7e-60;
tive 0; Mismatches 0;
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CURRENT FILING DATE: 2000-04-03
                    NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patentin version 3.1
SEQ ID NO 6
LENGTH: 108
                                                                                                                                                                                                                                            Conservative
                                                                                                       TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Homo sapiens
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Best Local Similarity
Matches 108; Conserv
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GENERAL INFORMATION:
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GENERAL INFORMATION:
GENERAL SELVENCES RELATING TO CANDIDA ALBICANS
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
GURRENT APPLICATION NUMBER: US/09/248,796A
CURRENT APPLICATION NUMBER: US 60/074,725
FRIOR APPLICATION NUMBER: US 60/096,409
FRIOR FILING DATE: 1998-02-13
FRIOR APPLICATION NUMBER: US 60/096,409
FRIOR FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208
SEQ ID NO 19598
ILENGTH: 118
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61.4%; Pred. No. 1.1e-33;
tive 12; Mismatches 26;
                                                                                                                                                                                                                                                        100.0%; Score 616; DB 4;
100.0%; Pred. No. 4.8e-60;
tive 0; Mismatches 0;
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FACEURATE INFORMATION
FAPELICANT: ISSAKANI, SARKIZ D.
APPLICANT: Brand, Jianing
APPLICANT: Sheung, Julie
APPLICANT: Rheung, Julie
APPLICANT: Rigel Pharmaceuticals, Inc.
TITLE OF INVENTION: Ubiquitin Ligase Assay
FILE REFERENCE: 021044-007010US
CURRENT APPLICATION NUMBER: US/09/826,312A
CURRENT PAPLICATION NUMBER: US/09/826,312A
FRIOR APPLICATION NUMBER: US/09/826,497
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 10811
LENGTH: 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 19598, Application US/09248796A; Patent No. 6747137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT ORGANISM: Candida albicans
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Best Local Similarity 61.4
Matches 62; Conservative
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                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
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                                                                                                                                                      ; TYPE: PRT
; ORGANISM: Human
US-09-949-016-10811
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TYPE: PRT
ORGANISM: Homo Sapiens
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ORGANISM: Homo sapiens
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APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Bougueleret, L.
APPLICANT: Bougueleret, L.
TITLE OF INVENTION: Complementary DNA's Encoding Proteins with Signal Peptides FILE REFERENCE: GENSET.050CP3
CURRENT APPLICATION NUMBER: 05/013,686
PRIOR APPLICATION NUMBER: 60/113,686
PRIOR APPLICATION NUMBER: 60/113,686
PRIOR APPLICATION NUMBER: 60/111,032
PRIOR PILING DATE: 1999-06-25
PRIOR FILING DATE: 1999-06-25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20 SGSTSG-GDKMFSLKKWNPVAMWSWDVECDTCAICRVQVMDACLRCQAEN---KQEDCVV 75
                                                                                                                                                                                                                                                                                                                                                                                    20 SGSTSG-GDKMFSLKKWNPVAMMSWDVECDTCAICRVQVMDACLRCQAEN---KQEDCVV
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46.6%; Score 287; DB 4; Length 113;
Best Local Similarity 49.5%; Pred. No. 5.1e-24;
Matches 48; Conservative 14; Mismatches 31; Indels
                                                                                                                                                                                                                                                         ch 46.6%; Score 287; DB 4; Length 113;
1 Similarity 49.5%; Pred. No. 5.1e-24;
48; Conservative 14; Mismatches 31; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Issakani, Sarkiz D.
APPLICANT: Huang, Jianing
APPLICANT: Shueng, Julie
APPLICANT: Shueng, Julie
ITLE OF INVENTION: UBIQUITIN LIGASE ASSAY
FILE REFERENCE: A-68613/RMS/JJD
CURRENT APPLICATION NUMBER: US/09/542,497A
CURRENT FILING DATE: 2000-04-03
CURRENT FILING DATE: 2000-04-03
SOFTWARE: PATENTIN VERSION 3.1
SEQ ID NO 8
                                                                                                                                                                                     OTHER INFORMATION: RING finger protein ROC2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 8, Application US/09542497A
Patent No. 6740495
PRIOR FILING DATE: 2000-04-03
                   NUMBER OF SEQ ID NOS: 21
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 8
LENGTH: 113
TYPE: PRT
ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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2 KVKIKCWNGVATWLWVANDENCGICRMAFNGCCPDCK-----VPGDDCPLVWGQCSHCFH 56
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                                                                                                                                                                                                                                                                               Length 84;
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Best Local Similarity 37.5%; Pred. No. 1.6e-15;
Matches 33; Conservative 17; Mismatches 30
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US-09-826-312A-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      81 FHCISRWLKTRQV---CPLDNREWEFQK 105
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APPLICANT: Issakani, Sarkiz D.
APPLICANT: Huang, Jianing
APPLICANT: Sheung, Julie
APPLICANT: Pray, Todd R.
APPLICANT: Pray, Todd R.
APPLICANT: Pray, Todd R.
TILLE OF INVENTION: Ubiquitin Ligase Assay,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Iseakani, Sarkiz D.
APPLICANT: Huang, Jianing
APPLICANT: Shueng, Julie
TITLE OF INVENTION: UBIQUITIN LIGASE ASSAY
FILE REPERENCE: A-68613/RMS/JJD
CURRENT APPLICATION NUMBER: US/09/542,497A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/826,312A CURRENT FILING DATE: 2001-04-03
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PRIOR APPLICATION NUMBER: US 09/542,497
PRIOR FILING DATE: 2000-04-03
NUMBER OF SEQ ID NOS: 21
SOFTWARE: PATENTIN VET. 2.1
FROM IN O S
PRIOR APPLICATION NUMBER: 09/469,099
PRIOR FILING DATE: 1999-12-21
NUMBER OF SEQ ID NOS: 123
SOFTWARE: Patent.pm
SEQ ID NO 77
LENGTH: 84
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Patent No. 6740495
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; LOCATION: -109..-1
US-09-621-976-5805
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NAME/KEY: UNSURE
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NAME/KEY: SIGNAL
LOCATION: -53..-1
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LENGTH: 112
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                                                                                                                                                                                         32.8%; Score 202; DB 4; Length 84; 36.4%; Pred. No. 7.4e-15; Artive 17; Mismatches 31; Indels
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Patent No. 6639063

GENERAL INPORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Glordano, J.Y.
TITLE OF INVENTION: ESTS and Encoded Human Proteins.
FILE REPRENCE: GENEST.054PR.2

CURRENT APPLICATION NUMBER: US/09/621,976

CURRENT FILING DATE: 2000-07-21

NUMBER OF SEQ ID NOS: 19335

SOFTWARE: Patent.pm

SEQ ID NO 5677
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Sequence 5805, Application US/09621976

Patent No. 6639063

GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Jobert, S.
TITLE OF INVENTION: ESTS and Encoded Human Proteins.
FILE REPERENCE: GENERI 0.054Pt2.
CURRENT APPLICATION WIMBER: US/09/621,976
CURRENT APPLICATION WIMBER: US/09/621,976

WIMBER OF SEQ ID NOS: 19335
SOFTWARE: PATENT PLING DATE: 2000-07-21
SEQ ID NO 5805
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CURRENT FILING DATE: 2000-04-03
NUMBER OF SEO ID NOS: 13
             NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patentin version 3.1
SEQ ID NO 5
LENGTH: 84
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Best Local Similarity 38.0%
Matches 30, Conservative
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Best Local Similarity 36.4
Matches 32; Conservative
                                                                                                                           ; ORGANISM: Homo sapiens
US-09-542-497A-5
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US-09-621-976-5677
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US-09-621-976-5677
                                                                                                           TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         48 HIMDLCIECOANOASATSEECTVAWGVCNHAFHFHCISRWL 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Jobert, S.
APPLICANT: Glordano, J.Y.
TITLE OF INVENTYON: ESTS and Encoded Human Proteins.
FILE REFERENCE: GENSET.054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT APPLICATION NUMBER: US/09/621,976
SUFFRENT FILING DATE: 2000.07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 5714
LENGTH: 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 17.1%; Score 105.5; DB 4; Best Local Similarity 36.6%; Pred. No. 0.00031; Matches 15; Conservative 8; Mismatches 13;
                                                                                                                                               30.0%; Score 185; DB 4; 38.0%; Pred. No. 7.4e-13;
                                                                                                                                                                                         13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 5714, Application US/09621976 Patent No. 6639063 GENERAL INFORMATION:
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PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR PLING DATE: 2000-10-03
PRIOR PELING DATE: 2000-10-03
PRIOR PELING DATE: 2000-09-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Dumas Milne Edwards, J.B. APPLICANT: Jobert, S.
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; OTHER INFORMATION: Xaa = Glu,Gln
US-09-621-976-5714
                                                                                                                                                                                                                                                                                                                     81 FHCISRWLKTROV---CPL 96
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57 MHCILKWLHAQQVQQHCPM 75
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Best Local Similarity 38.0%
Matches 30; Conservative
TYPE: PRT
ORGANISM: Homo sapiens
PEATURE:
NAME/KEY: SIGNAL
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ORGANISM: Homo sapiens
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Sequence 6249, Application US/09949016
; Sequence 6249, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
    APPLICANT: VERYER, J. Craig et al.
    APPLICANT: VERYER, J. Craig et al.
    TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REPRENCATION NUMBER: US/09/949,016
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT PILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR FILING DATE: 2000-10-03
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOPTWARE: FREESEQ for Windows Version 4.0
; SEQ ID NO 6249
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14.6%; Score 90; DB 4; Length 195;
Best Local Similarity 26.3%; Pred. No. 0.034;
Matches 25; Conservative 11; Mismatches 15; Indels 44; Gaps
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14.0%; Score 86; DB 4; Length 326;
Best Local Similarity 30.2%; Pred. No. 0.17;
Matches 19; Conservative 11; Mismatches 23; Indels 10; Gaps
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SOFTWARE: PastSEQ for Windows Version 4.0
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; ORGANISM: Human
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; ORGANISM: Human
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N-PSDB; AAA96882.
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Maximum Match 100%
Listing first 45 summaries
                                  - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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geneseqp2003as:*
geneseqp2003bs:*
geneseqp20048:*
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290.5 287 287 287	287 285 283	283 282 282	282 282 282	282 282 282	274	255.5
26 28 29 29	30 31 32	3 3 3 3 4 3	36 37 38	3 4 4 1 1	4 4 4 2 6 4	45

ALIGNMENTS

Amino acid sequence of human ring finger protein ROC1. AAB19160 standard; protein; 108 AA

ROC1; ROC2; cullin; ring finger protein; APC11; APC complex; SCF pathway; cullin dependent ubiquitin ligase; CDK inhibitor Sic1 degradation;

31-MAR-2000; 2000WO-US008592.

(UYNC-) UNIV NORTH CAROLINA.

Novel nucleic acid encoding cullin regulating ring finger proteins, termed as ROC proteins similar to anaphase-promoting complex 11, for therapeutic and diagnostic use.

Claim 9; Fig 2A; 83pp; English

The present sequence represents a human ROC1 ring finger protein. The specification also describes human ROC2. ROC1 and ROC2 are similar to APC11, a subunit of the APC complex. The proteins stimulate cullin dependent ubiquitin ligase activity. ROC1 functions in vivo as an essential regulator of CDK inhibitor Sic1 degradation by the SCF (undefined) pathway. ROC proteins are useful for screening bioactive agents that interfere with the binding of ROC proteins with cullin proteins. Pharmaceutical formulations comprising ROC proteins are useful for diagnostic and therapeutic purposes, preferably for diagnosing and treating tumours

Pred. No. 3.8e-64;

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                                                                                                                                                              1 MAAAMDVDTPSGTNSGAGKKRFEVKKWNAVALWAWDIVVDNCAICRNHIMDLCIECQANQ 60
                                                                                                                                                                                                          1 MAAAMDVDTPSGTNSGAGKKRFEVKKWNAVALWAWDIVVDNCAICRNHIMDLCIECQANQ 60
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                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cullin-interacting RING-H2 finger protein, Ring box protein; Rbx1, tumour suppressor; carcinoma; Ring box associated carcinoma; von Hippel-Lindau complex; ubiquitin conjugation; renal carcinoma; cerebellar hemangioblastoma; hemangioma; retinal angiomata;
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                                                                Length 108;
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                                                             Score 616; DB 3;
Pred. No. 3.8e-64;
                                                                                                                 Mismatches
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                                                                  Query Match 100.
Best Local Similarity 100.
Matches 108; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 108 AA;
                        Sequence 108 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31-AUG-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB08813;
                                                                                                                                                                                                                                                                                                                                                                             RESULT 2
AAB08813
ID AAB08813

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DB 3; Length 108;

100.0%; Score 616;

Query Match

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence is a polypeptide encoded by one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer cDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design expression and secretion vectors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9
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                                                                                                                                             1 MAAAMDVDTPSGTNSGAGKKRFEVKKWNAVALWAWDIVVDNCAICRNHIMDLCIECQANQ 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   expressed sequence tag; secreted protein; cDNA isolation;
                                                                                                          1 MAAAMDVDTPSGTNSGAGKKRFEVKKWNAVALWAWDIVVDNCAICRNHIMDLCIECQANQ
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                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5'ESTs and for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and £0'
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                                                                                                                                                                                                                       61 ASATSEECTVAWGVCNHAFHFHCISRWLKTRQVCPLDNREWEFQKYGH 108
                                                                                                                                                                                                                                                                            108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          claim 13, SEQ ID NO 7971, 71pp + Sequence Listing; English.
                                                                                                                                                                                                                                                          61 ASATSEECTVAMGVCNHAFHFHCISRWLKTRQVCPLDNREWEFQKYGH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                  Indels
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100.0%; Pred. No. 3.8e-64;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Giordano J;
                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human secreted protein, SEQ ID NO: 7971.
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                                                                                                                                                                                                                                                                                                                                                                                                                            AAG03890 standard; protein; 108 AA
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100.08; Fig.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gene therapy; chromosome mapping.
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Matches 108; Conservative
                                                     108; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Dumas Milne Edwards J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2000-500381/45.
                       Best Local Similarity
Matches 108; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; AAC03896
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (GEST ) GENSET
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAG03890;
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The sequences given in AAB47596-602 are proteins which may be used in the method of the invention for assaying ubiquitin ligase activity. The method comprises combining under conditions that favour ubiquitin ligase activity, tagl-ubiquitin 21 (ubiquitin ligase) and measuring the amount of tagl-ubiquitin bound to the B3. The method is useful for assaying ubiquitin ligase activity and ubiquitin enzyme activity which is useful for identifying ubiquiting modulator. The method comprises combining tagl-ubiquitin, the modulator, E1, E2 and tag2-E3 and measuring the amount of tagl-ubiquitin, bound to tag3-E2 and measuring the amount of tagl-ubiquitin bound to tag3-E2 and measuring the amount of tagl-ubiquitin ligase activity is measured chiquitin bound to tag3-E2. Ubiquitin ligase activity is measured analysis such as separating ligated from unligated material in an SDS-DAGE procedure. This allows multi-well array analysis and high throughput screening techniques for modulators of ubiquitination activity. The method also allows the analysis of many different combinations of E3 components and E2/E3 combinations without requiring prior identification of specific target substrates. Ubiquitin is labeled, directly or indirectly and this allows for easy and rapid detection and measurement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Assaying ubiquitin ligase activity for identifying modulators of ubiquitination, by combining ubiquitin, ubiquitin activating conjugating enzyme, ubiquitin ligase and measuring amount of ubiquitin bound to the
                                                                                                                                                                                            Assay, ubiquitin ligase, tagl-ubiquitin, El, E2;
ubiquitin activating enzyme, ubiquitin conjugating enzyme;
ubiquitin ligase, ubiquitination modulator.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 616; DB 4;
100.0%; Pred. No. 3.8e-64;
iive 0; Mismatches 0;
                                    AAB47599 standard; protein; 108 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sheung J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 1; Fig 11; 98pp; English.
                                                                                                                                                                                                                                                                                                                                                                                            03-APR-2001; 2001WO-US010906.
                                                                                                                                                                                                                                                                                                                                                                                                                                03-APR-2000; 2000US-00542497
                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (RIGE-) RIGEL PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Huang J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          of ligated ubiquitin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-626445/72.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 108 AA;
                                                                                                                                                                                                                                                                                                               WO200175145-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Issakani SD,
                                                                                                                                                                                                                                                                         Unidentified
                                                                                                                   07-JAN-2002
                                                                            AAB47599;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ligase.
                                                                                                                                                       ROC1.
RESULT 4
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Pray TR;

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Assay for ubiquitin ligase activity, useful for identifying modulators,
by measuring binding of labeled ubiquitin to ubiquitin ligase.
                                                                                                                                                                                                                Ubiquitin ligase, UL; tagl-ubiquitin; El; ubiquitin-activating enzyme;
E2; ubiquitin-conjugating enzyme/ubiquitin carrier protein; E3; human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MAAAMDVDTPSGTNSGAGKKRFEVKKWNAVALWAWDIVVDNCAICRNHIMDLCIECQANQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          which comprises incubating tag1-ubiquitin, El (ubiquitin-activating enzyme), E2 (ubiquitin-conjugating enzyme/ubiquitin carrier protein) E3 (UL) and measuring the amount of tag1-ubiquitin bound to E3. The method is particularly used to screen for modulators of UL activity. present sequence is human RING finger protein, ROC1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to an assay for ubiquitin ligase (UL) activity
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ASATSEECTVAMGVCNHAFHFULSRWLKTRQVCPLDNREWEFQKYGH 108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 108;
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100.0%; Pred. No. 3.8e-64;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ubiquitin; Mdm2; p53; RING finger protein; ROC1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure, Fig 11; 56pp, English.
                                                                                                                                                                                     Human RING finger protein, ROC1.
                                                                                                   AAE24620 standard; protein; 108
                                                                                                                                                                                                                                                                                                                                                            03-APR-2001; 2001US-00826312.
                                                                                                                                                                                                                                                                                                                                                                                          03-APR-2000; 2000US-00542497.
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                                                                                                                                                                                                                                                                                                                                                                                                                      (RIGE-) RIGEL PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Huang J,
                                                                                                                                                                                                                                            RING finger protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2002-488718/52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 108 AA;
                                                                                                                                                                                                                                                                                                     US2002042083-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                 ssakani SD,
                                                                                                                                                                                                                                                                            sapiens
                                                                                                                                                         22-OCT-2002
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                                                                                                                                                                                                                                                                                                                                 11-APR-2002.
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                                                                                                                              AAE24620;
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Matches 108; Conservative

1 MAAAMDVDTPSGTNSGAGKKRFEVKKWNAVALWAWDIVVDNCAICRNHIMDLCIECQANQ 60 1 MAAAMDVDTPSGTNSGAGKKRFEVKKWNAVALWAWDIVVDNCAICRNHIMDLCIECQANQ

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and

US2003104474-A1

05-JUN-2003

Unidentified

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that are enzymatic components of ubiquitin-mediated protectives are enzymatic components of ubiquitin-mediated protectives. Specifically, it refers to a method for identifying ubiquitin-activating, conjugating agents that work to modulate the attachment of a ubiquitin moiety to at least one other ubiquitin agent. The method comprises combining a first ubiquitin agent, candidate agent and ubiquitin moiety, and subsequently assaying for the attachment of a ubiquitin moiety, to the first agent. The present invention does not require a ubiquitin target protein and allows the analysis of many different combinations of ubiquitin agents, without requiring the identification of specific target proteins. Consequently, this method is easy, applicable for high-throughput sereening applications and so can rapidly detect the activity of ubiquitin agents. This polypeptide sequence is the RING finger protein ROC1, an E3 ubiquitin ligating agent
                                                                                                                                                                                                                                                                                                                                         Assaying agent that modulates attachment of ubiquitin moiety to ubiquiting agent, by combining first ubiquitin agent, candidate agent and ubiquitin moiety, and assaying agent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MAAAMDVDTPSGTNSGAGKKRFEVKKWNAVALWAWDIVVDNCAICRNHIMDLCIECQANQ 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tumour-associated antigenic target (TAT) polypeptide FRO83289, SEQ:6073.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tumour-associated antigenic target; TAT; human; overexpression; cancer; tumour; diagnosis; cell proliferative disorder; breast cancer; colorectal cancer; lung cancer; ovarian cancer; liver cancer; central nervous system cancer; bladder cancer; pancreatic cancer; cervical cancer; melanoma; leukaemia; hybridisation probe; chromosome identification; chromosome mapping; gene mapping;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This invention relates to a novel method for assaying ubiquitin agents that are enzymatic components of ubiquitin-mediated proteolysis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 ASATSEECTVAWGVCNHAFHFICISRWLKTRQVCPLDNREWEFQKYGH 108
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                                                                                                                                                                                                                                                    Sheung J,
                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Fig 11; 95pp; English.
                  2002US-00091139.
2002US-00091174.
2002US-00108767.
2001US-0291836P
                                                                                     2002US-00109460
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Best Local Similarity 100.
Matches 108; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gene therapy; cytostatic.
                                                                                                                                                                                                                                                    Huang J,
                                                                                                                                (ISSA/) ISSAKANI S D (HUAN/) HUANG J. (SHEU/) SHEUNG J. (PRAY/) PRAY T R.
                                                                                                                                                                                                                                                                                              WPI; 2003-810851/76.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 108 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO2004030615-A2
                  04-MAR-2002;
04-MAR-2002;
26-MAR-2002;
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                                                                                                                                                                                                                                                    Issakani SD,
                                                                                     26-MAR-2002;
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ABM82365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence represents a method of assaying for a candidate agent that modulates the attachment of a ubiquitin moiety to an Mdm2 protein. The method is useful for assaying for a candidate agent that modulates the attachment of a ubiquitin moiety to an Mdm2 or p53 protein. The present sequence represents the amino acid sequence of RING finger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Assaying for candidate agent that modulates attachment of ubiquitin moiety to Mdm2 protein comprises combining ubiquitin agent comprising ubiquitin moiety, Mdm2 protein, and candidate agent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ROC1; ubiquitin-mediated proteolysis; high-throughput screening;
E3 ubiquitin ligating agent; RING finger.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 616; DB 7; Length 108; 100.0%; Pred. No. 3.8e-64; cive 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RING finger protein ROC1, an E3 ubiquitin ligating agent.
                                                                                                                                                                                                                                                                                                                                                                                                                   Pray TR;
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                                                                                                                                                                                                                                                                                                                                                                                                                   Sheung J,
                                                                                                                                                                                                       03-APR-2000; 2000US-00542487.
03-APR-2001; 2001US-00826312.
04-MAR-2002; 2002US-0091139.
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                                                                                                                                                            26-MAR-2002; 2002US-00108767
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20-MAY-2002; 2002US-00152156
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                                                                                                                                                                                                                                                                                                   ISSAKANI S D.
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                                                                                                                                                                                                                                                                                                                    HUANG J.
SHEUNG J.
PRAY T R.
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Sequence 108 AA;

Query Match

Matches

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protein ROC1.

[ssakani SD,

(ISSA/) 1 (HUAN/) H (SHEU/) 8 PRAY/) US2003108947-A1

12-JUN-2003

Unidentified

12-FEB-2004

ADF17866;

RESULT

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Gaps .. 0 S

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The invention relates to human tumour-associated antigenic target (TAT) polypeptides, and their related nucleic acids. The TAT polypeptides are overexpressed in cancer tissues compared to normal tissues, and may thus serve as effective targets for the diagnosis and treatment of cancer in mammals. The invention also relates to nucleic acid and polypeptide polypeptides at least 80% identical to the TAT nucleic acids and polypeptide polypeptides expression vectors and host calls comprising a TAT nucleic acid; an antibody specific for a TAT polypeptide; a peptide or organic molecule which binds to a TAT polypeptide; fusion proteins comprising a TAT polypeptide; and methods and compositions for the treatment or diagnosis of cancer in mammals. TAT polypeptides, nucleic acids, antibodies, antagonists, binding molecules and compositions are useful for diagnosing or treating a cell proliferative disorder associated with increased TAT expression, particularly cancers such as breast cancer, colorectal cancer, lung cancer, cervical cancer, liver cancer, bladder cancer, pancreatic cancer, cervical cancer, cancers of the central cancer, melanoma and leukaemia. TAT nucleic acids may further be used as hybridisation and in gene therapy. The present sequence represents a TAT polypeptide of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MAAAMDVDTPSGTNSGAGKKRFEVKKWNAVALWAWDIVVDNCAICRNHIMDLCIECQANQ 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human protein of a TNF-alpha signalling pathway protein complex Seg 146.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein complex; tumour necrosis factor-alpha signalling pathway; TNP-alpha; chronic inflammatory disease; rheumatoid arthritis; inflammatory bowel disease; infectious sisease; septic shock; bacterial infection; neurological disease; stroke-induced inflammation; neurodegenerative disease; cancer; antiinflammatory; antiarthritic; antirheumatic; cytostatic; antibacterial; gene therapy; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MAAAMDVDTPSGTNSGAGKKRFEVKKWNAVALWAWDIVVDNCAICRNHIMDLCIECQANQ
                                                                                                                                                                                                                                                                                                            New tumor-associated antigenic target polypeptides and nucleic acids, useful in preparing a medicament for treating or detecting a proliferative disorder, e.g. breast, lung, colorectal, ovarian or
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                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 12; SEQ ID NO 6073; 7273pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADS88291 standard; protein; 108 AA
                                                                29-SEP-2003; 2003WO-US028547
                                                                                                          02-OCT-2002; 2002US-0414971P.
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                                                                                                                                                                                                  Wu TD, Zhang Z, Zhou Y;
                                                                                                                                                                                                                                                                                                                                                                               prostate cancer or tumor.
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Matches 108; Conservative
                                                                                                                                                      (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                         WPI; 2004-347921/32.
N-PSDB; ACN40951.
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                       15-APR-2004
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This invention relates to novel protein complexes of the tumour necrosis factor-alpha (TNF-alpha) signalling pathway. Specifically, it refers to methods for preparing these complexes comprising at least two component proteins, as well as screening methods to identify modulators of the proteins, as well as screening methods to identify modulators of the present invention describes a protein complex and kit that are useful for diagnosing, prognosing or treating chronic inflammatory diseases such as recording arthritis and inflammatory bowel disease, infectious diseases such as septic shock and bacterial infections; neurological diseases such as stroke-induced inflammation in neurons; neurological diseases such as stroke-induced inflammation in neurons; neurological diseases and cancer. Accordingly, these complexes can be used for the development of pharmaceutical compositions that exhibit antinflammatory, antiarthritic, antirheumatic, cytostatic and antibacterial activities and can be used for gene therapy purposes. In particular, the invention further provides is INNA-oligonucleotides useful for inhibiting protein expression for in vitro or cell culture assays. This polypeptide is a human protein that can be used in combination with other proteins provided in the photonic control of the inventor protein that the inventor in the complexes of the INF-alpha signalling pathway
                                                                                                                                                                                                                                                                                                                                                                                       New protein complex comprising at least one first and second protein of
the Tumor Necrosis Factor-alpha(TNF-alpha)-signaling pathway, useful for
diagnosing or treating inflammation, neurological diseases, infectious
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                                                                                                                                                                                                                                                                                       Bauer A,
                                                                                                                                                                                                                                                                                     Bauch A, Ruffner H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example; SEQ ID NO 146; 1980pp; English.
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                                                                                                                                          24-SEP-2003; 2003WO-EP050655.
                                                                                                                                                                                   2002EP-00021809
                                                                                                                                                                                                    10-FEB-2003; 2003EP-00100274
                                                                                                                                                                                                                                                                                                      Kruse U;
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                                                                                                                                                                                                                                                                                                                                                 WPI; 2004-348460/32.
                                                                                                                                                                                                                                            (CELL-) CELLZOME AG.
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                                                         WO2004035783-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 108 AA;
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                     Homo sapiens.
                                                                                                                                                                               26-SEP-2002;
                                                                                                  29-APR-2004.
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Gaps

Drosophila; developmental biology; cell signalling; insecticide;

pharmaceutical.

Drosophila melanogaster polypeptide SEQ ID NO 31032.

(first entry)

26-MAR-2002

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9905-0139461P
9905-0139462P
9905-0139463P
9905-0139763P
9905-0139763P
9905-0139817P
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99US-014290P.
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          99US-0123180P.
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25-FEB-1999;
05-MAR-1999;
09-MAR-1999;
23-MAR-1999;
25-MAR-1999;
01-APR-1999;
06-APR-1999;
06-APR-1999;
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23-APR-1999;
28-APR-1999;
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16-JUN-1
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                                                                                                                                                                                                                                                                                                                                                                                           -NDD-70
    The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher enkaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MEVDEDGYEVPSSSSKG-DKKRFEVKKWNAVALWAWDIVVDNCAICRNHIMDLCIECQAN 59
                                                                                                                                                                                                                                                                                                                                                                                                                                   MDVD----TPSGTNSGAGKKRFEVKKWNAVALWAWDIVVDNCAICRNHIMDLCIECQAN 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter;
                                                                                                                                                                                             New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; SEQ ID NO 31032; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                          Query Match 86.7%; Score 534; DB 4; Length 108; Best Local Similarity 87.2%; Pred. No. 1.6e-54; Matches 95; Conservative 4; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Arabidopsis thaliana protein fragment SEQ ID NO: 26148.
                                                                                                                                             Li PWD, Myers EW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAG23004 standard; protein; 118 AA.
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                                                                       23-MAR-2001; 2001WO-US009231
                                                                                           23-MAR-2000; 2000US-0191637P.
11-JUL-2000; 2000US-00614150.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17-OCT-2000 (first entry)
           Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   termination sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Arabidopsis thaliana
                                                                                                                                             Venter JC, Adams M,
                                                                                                                                                                 WPI; 2001-656860/75.
                                                                                                                         (PEKE ) PE CORP NY
                                                                                                                                                                          N-PSDB; ABL12183
                                                                                                                                                                                                                                                                                                                                                                        Sequence 108 AA;
                                WO200171042-A2
                                                                                                                                                                                                                    interactions.
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                                                     27-SEP-2001
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9905-015108P
99US-0143542P
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02-AUG-1999;
02-AUG-1999;
03-AUG-1999;
04-AUG-1999;
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06-AUG-1999;
09-AUG-1999;
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13-AUG-1999;
16-AUG-1999;
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18-AUG-1999;
20-AUG-1999;
20-AUG-1999;
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23-AUG-1999;
23-AUG-1999;
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27-AUG-1999;
27-AUG-1999;
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30-AUG-1999;
31-AUG-1999;
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16-SEP-1999;
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12-AUG-1999
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22-SEP-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAMDVDT---PSG-----TNSGAGKKRFEVKKWNAVALWAWDIVVDNCAICRNHIMD
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                         11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Arabidopsis thaliana protein fragment SEQ ID NO: 26149.
                                                                                                                                                                                                                                                                                                                                                                                                                               83.5%; Score 514.5; DB 3
larity 78.6%; Pred. No. 3.5e-52;
Conservative 6; Mismatches 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAG23005 standard; protein; 109 AA
99US-0157117P

99US-015723P

99US-0158023P

99US-0158234P

99US-0159234P

99US-0159234P

99US-0159234P

99US-0159234P

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99US-0160981P
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99US-0123180P.
99US-0123548P.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         termination sequence
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05-MAR-1999;
09-MAR-1999;
04-0CT-1999,
05-0CT-1999,
06-0CT-1999,
08-0CT-1999,
13-0CT-1999,
13-0CT-1999,
14-0CT-1999,
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12-0CT-1999,
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- MAR 1999 - MAR 1999 - MAR 1999 1 - APR 1999 5 - APR 1999 5 - APR 1999 9 - APR 1999 1 - APR 1999 3 - APR 1999 3 - APR 1999 9 - APR 1999	05-MAY-1999; 06-MAY-1999; 07-MAY-1999; 11-MAY-1999; 14-MAY-1999; 14-MAY-1999; 14-MAY-1999; 19-MAY-1999; 20-MAY-1999; 21-MAY-1999; 21-MAY-1999; 22-MAY-1999; 22-MAY-1999; 22-MAY-1999; 01-JUN-1999; 01-JUN-1999; 01-JUN-1999; 01-JUN-1999; 01-JUN-1999; 01-JUN-1999; 116-JUN-1999; 116-JUN-1999; 118-JUN-1999; 118-JUN-1999; 118-JUN-1999; 118-JUN-1999; 118-JUN-1999; 118-JUN-1999; 118-JUN-1999; 118-JUN-1999; 118-JUN-1999;	8 - JUN - 1999 8 - UUN - 1999 8 - UUN - 1999 8 - UUN - 1999 8 - UUN - 1999 9 - UUN - 1999 3 - UUN - 1999 9 - UUN - 1999 9 - UUN - 1999 9 - UUL - 1999 6 - UUL - 1999 8 - UUL - 1999 9 - UUL - 1999 8 - UUL - 1999 7 - UUL - 1999 8 - UUL - 1999
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41004410	JUS-0144085P	US-0144325P	JUS-0144331P	9US-0144332P	OS-0144334P	ONS-0144335P	99US-0144352P.	US-0144884P	9US-0144814P	70S-0145086F	9US-0145085P	9US-0145087P	9US-0145089P 9HS-0145192D	9US-0145145P	9US-0145218P	9US-0145224P	9US-01452/6F 9US-0145913P	OUS-0145918P	9US-0145919P	9US-0145951P	9US-0146386F 9US-0146388P	OUS-0146389P	9US-0147038P	9US-0147204P	9US-0147192P	9US-0147260P	9US-0147303P 9US-0147416P	9US-0147493P	9US-0147935P	9US-01481/1F 9US-0148319P	9US-0148341P	9US-0148565P	9US-0149368P	9US-0149175P	9US-0149426P 9US-0149722P	9US-0149723P	9US-0149929P	9US-01499U2F 9US-0149930P	9US-0150566P	9US-0150884P 9US-0151065P	9US-0151066P	9US-0151080P	90S-0151303F 91IS-0151438P	9US-0151930P	9US-0152363P	9US-0153070E	9US-0154018F	9US-0154039P	9US-0154779F 9US-0155139F	9US-0155486P	9US-0155659F	9US-0156458P	9US-0157117P	9US-0157753P	9US-0157865P
	5-JUL-1999	9-JUL-1999	9-JUL-1999	9-JUL-1999	9-JUL-1999	9-JUL-1999	20-JUL-1999; 20-JH:-1999;	0-JUL-1999	1-JUL-1999	1-00E-1999 1-:TIT:-1999	2-JUL-1999	2-JUL-1999	2-JUL-1999 2-JUL-1999	3-JUL-1999	3-JUL-1999	3-JUL-1999	6-JUE-1999 6-JUE-1999	7-JUL-1999	7-JUL-1999	8-JUL-1999	2-AUG-1999 2-AUG-1999	2-AUG-1999	3-AUG-1999	4-AUG-1999	4 - AUG - 1999 5 - AUG - 1999	5-AUG-1999	6-AUG-1999 6-AUG-1999	9-AUG-1999	9-AUG-1999	0-AUG-1999 1-AUG-1999	2-AUG-1999	3-AUG-1999	5-AUG-1999 6-AUG-1999	7-AUG-1999	8-AUG-1999	0-AUG-1999	0-AUG-1999	3-AUG-1999 3-AUG-1999	5-AUG-1999	6-AUG-1999 7-AUG-1999	7-AUG-1999	7-AUG-1999	0-AUG-1999 1-AIIG-1999	1-SEP-1999	7-SEP-1999	0-SEF-1999 3-SEP-1999	5-SEP-1999	6-SEP-1999	0-SEP-1999 2-SEP-1999	3-SEP-1999	4-SEP-1999	8-SEP-1999	4-0CT-199	5-0CT-199	6-0CT-199
í	7. T	. A.	PR	ሟ ር	7 Y	PR	ሟ <u>ሮ</u>	. K.	R	ች <u>የ</u>	PR	PR 1	PR PR	P. P.	PR	PR	7.4 G	PR	PR	ዋ ያ	7. G	PR	PR	PR	PR PR	PR	PR G	PR PR	PR	X G	PR	PR G	P. P. R.	PR	PR G	£ &	PR R	Y K	PR	PR PR	PR.	K 1	P. P.	PR.	PR E	Y P	PR	PR.	ም አ	. K	PR	다. 다.	P. P.	PR	PR

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1.8
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                                                                                                                              The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL061840-ABL16175) and the encoded proteins (ABB57737-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                           New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell interactions.
                                                                                                                                                                                                                                                                                                                                                                                 5 MDVDTPSGTNSG----AGKKRFEVKKWNAVALWAWDIVVDNCAICRNHIMDLCIECQANQ
                                                                                                                                                                                                                                                                                                                                                                                                      16 MDFNDEEPSCSGGAVQARTERFVVKKWVAHAMWGWDVAVDNCAICRNHIMNLCIECQAD-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cullin interacting RING-H2 finger protein, a component of von Hippel-Lindau tumor suppressor complex and Skpl-Cdc33p-F-box protein (SCF) ubiquitin ligase, useful for diagnosing and treating Ring box protein associated carcinomas.
                                                                                                                                                                                                                                                                                                                                                      Gape
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cullin-interacting RING-H2 finger protein, Ring box protein, Rbx1, tumour suppressor; carcinoma, Ring box associated carcinoma; von Hippel-Lindau complex; ubiquitin conjugation; renal carcinoma; cerebellar hemangioblascoma; hemangioma; retinal angiomata;
                                                                                                                                                                                                                                                                                                                                                    2
                                                                                                      Disclosure; SEQ ID NO 25119; 21pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                      65.0%; Score 400.5; DB 4; Length 122; 65.4%; Pred. No. 8.7e-39; ive 13; Mismatches 19; Indels 5
                                                                                                                                                                                                                                                                                                                                                                                                                                          61 ASATSEECTVAWGVCNHAFHFHCISRWLKTROVCPLDNREWEFOKYG 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                         BINANQDECTVAMGECNHAFHYHCIARWLKTRLVCPLDNKEWVYQKYG 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A yeast cullin-interacting RING-H2 finger protein (Rbx1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kamura T;
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Best Local Similarity 65.44
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   WPI; 2001-656860/75.
N-PSDB; ABL10212.
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                                                                                                                                                                                                                                                                                             Sequence 122 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Drosophila; developmental biology; cell signalling; insecticide;
pharmaceutical.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 109
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Pred. No. 8.1e-52,
5, Mismatches 6, Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AWGVCNHAFHFHCISRWLKTRQVCPLDNSEWEFQKYGH 109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AWGVCNHAFHFHCISRWLKTRQVCPLDNREWEFQKYGH 108
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99US-0158029P.
99US-015832P.
99US-0158369P.
99US-015923P.
99US-0159294P.
99US-0159232P.
                                                                                                               990S-0159331P.
990S-0159637P.
99US-0159638P.
99US-0169584P.
99US-0160767P.
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99US-0161359P.
99US-0161360P.
99US-0161361P.
99US-0161920P.
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99US-0160814P.
99US-0160815P.
99US-0160980P.
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99US-0160989P.
99US-0161404P.
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99US-0161993P.
99US-0162142P.
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                                                                                                                                                                                                       99US-0160768P
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88.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 88.8
1es 87; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Adams M,
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                            12-0CT-1999;
13-0CT-1999;
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12-0CT-1999;
12-0CT-1999;
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26-OCT-1999;
26-OCT-1999;
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28-0CT-1999;
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-007-1
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Matches
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CC The present sequence represents a yeast cullin-interacting RING-H2 finger protein (Ring box protein), designated Rbx1. The human Rbx1 polypeptide is a tumour suppressor. Human Rbx1 is useful for diagnosing a parient to certain carcinomas. It is also useful for treating Ring box protein associated carcinomas or augmenting metabolically deficient system in animals. Human Rbx1 is also useful for evaluating the effectiveness of a therapeutic treatment for Ring box associated carcinomas. Human Rbx1 can be used to screen for agents which augment or inhibit the activity of other cullin-containing ubiquitin conjugation of ubiquitin or ubiquitin. It we proteins to various sets of target proteins. Carcinomas which may be treated include renal carcinomas, cerebellar hemangioblastomas and hemangiomas, retinal
  Disclosure; Page 34-35; 37pp; English.
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Sequence 121 AA;

54 63 5 MDVDTPSGTNSGAG-----KKRFEVKKWNAVALWAWDIVVDNCAICRNHIMDLCI Gaps ECOANQASATSEECTVAWGVCNHAFHFHCISRWLKTRQVCPLDNREWEFQKYG 107 68 ECQPKAMTDTDNECVAAMGVCNHAPHIHCINKWIKTRDACPLDNQPWQLARCG 120 29; Indels 10; 62.5%; Score 385; DB 3; Length 121; 56.6%; Pred. No. 5.7e-37; ive 10; Mismatches 29; Indels 1 Local Similarity 56.6 es 64; Conservative æ 55 Query Match 셤 ò ò

sea-squirt; zinc finger protein; gene detection; drug development; zinc finger protein-associated disease. Sea-squirt (Ciona intestinalis) zinc finger protein #67 ADP22560 standard; protein; 59 (first entry) 12-AUG-2004 ADP22560; RESULT 15
ADP22560
XX
AC ADP22
XX
DT 12-AU
XX
DE Sea-8
XX
DE Sea-8
XX
SEA-8

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31-JUL-2002; 2002JP-00222484. JP2004057126-A. 26-FEB-2004

Ciona intestinalis.

(KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN

31-JUL-2002; 2002JP-00222484

WPI; 2004-208711/20 N-PSDB; ADP22559 Novel gene encoding zinc finger protein, useful as probe in gene detecting instruments and in development of drug for treating zinc finger

The invention comprises the amino acid and coding sequences of sea-squirt (Ciona intestinalis) zinc finger proteins. The DNA and protein sequences of the invention are useful in a gene detecting instrument. The DNA and protein sequences of the invention are useful in the development of drugs for the treatment of zinc finger protein-associated diseases. The present amino acid sequence represents a sea-squirt zinc finger protein of the Claim 1; SEQ ID NO 134; 972pp; Japanese. protein associated diseases. invention.

Sequence 59 AA; XX SS

Gaps ; 0 Length 59; Score 336; DB 8; Lengtn >>,
Pred. No. 1.4e-31; 1; Mismatches 54.5%; 98.3%; 57; Conservative Query Match Best Local Similarity Matches 57; Conserv

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50 MDLCIECQANQASATSEECTVAWGVCNHAFHFHCISRWLKTRQVCPLDNREWEFQKYG 107 1 MDLCIECQANQASAISDECTVAMGVCNHAFHFHCISRWLKTRQVCPLDNRBWEFQKYG 58 ઠે g

completed: June 23, 2005, 15:26:42 : 165 secs Job time Search

Perfect score:

Sequence:

OM protein

Run on:

Scoring table:

Searched:

Database

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Sequence 191492, Sequence 291051, Sequence 230014, Sequence 316213, Sequence 316213, Sequence 316213, Sequence 626, App Sequence 8, Appli Sequence 8, Appli Sequence 8, Appli Sequence 24228, Sequence 24228, Sequence 620, App Sequence 620, App Sequence 120, App Sequence 1214, Ap Sequence 1214, Appli Sequence 1214, A
                                                                                                                                                                                                                                                                                                                                                                       Sequence 253860,
Sequence 51781, A
Sequence 5, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MAAAMDVDTPSGTNSGAGKKRFEVKKWNAVALWAWDIVVDNCAICRNHIMDLCIECQANQ
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                                                                                                                    US-09-764-864-826
US-09-764-864-1285
US-10-424-599-238320
US-09-826-312-8
US-10-108-767-8
4 US-10-152-156-8
4 US-10-152-156-8
5 US-10-424-599-244228
US-10-424-599-244079
US-09-925-298-620
           US-10-424-599-148915
US-10-425-115-191492
US-10-425-115-291051
US-10-913-937-2
US-10-425-115-352839
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US-10-425-115-352839
US-10-425-115-35283
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US-09-764-864-1284
US-09-978-3604-409
US-10-315-664-77
US-10-221-625-94
US-10-424-599-253860
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US-10-276-774-2678
US-10-264-049-2937
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US-10-835-096-5
US-10-264-049-2926
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APPLICANT: ISSAKAII, Sarkiz D.
APPLICANT: Sheung, Jianing
APPLICANT: Sheung, Julie
APPLICANT: Pray, Todd R.
TITLE OF INVENTION: UBIQUITIN LIGASE ASSAY
FILE REFERENCE: A-66613-1/RMS/JJD
CURRENT APPLICATION NUMBER: US/09/826,312
CURRENT FILING DATE: 2001-04-03
PRIOR APPLICATION NUMBER: US 09/542,497
PRIOR FILING DATE: 2000-04-03
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PATENTIN VERSION 3.1
SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 6, Application US/09826312
Patent No. US20020042083A1
GENERAL INFORMATION:
Matches 108; Conservative
TYPE: PRT
ORGANISM: Homo sapiens
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US-09-826-312-6
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Sequence 1, Appli
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Sequence 148916,
Sequence 201494,
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                                                                                                           (without alignments)
262.856 Million cell updates/sec
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                                                                                                                                                                              1 MAAAMDVDTPSGTNSGAGKK......KTRQVCPLDNREWEFQKYGH 108
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                                                                                                                                                                                                                                                                                                                                                                                                               June 23, 2005, 15:29:52 ; Search time 158 Seconds
              GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-10-152-156-6
US-10-913-937-1
US-10-913-937-6
US-10-131-937-6
US-10-767-701-48916
US-10-424-599-148916
US-10-424-599-148916
US-10-767-701-48916
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US-10-767-701-48916
US-10-748-115-201494
US-10-744-599-221431
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Maximum Match 100%
Listing first 45 summaries
                                                                   - protein search, using sw model
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Maximum DB seq length: 200000000
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sequence 1, Application US/10913937

publication No. US20050019813A1

general Information:

general Informatio
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                                                                                                                                                                                     Length 108;
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                                                                                                                                                                                  Query Match 100.0%; Score 616; DB 14; Best Local Similarity 100.0%; Pred. No. 7.7e-60; Matches 108; Conservative 0; Mismatches 0;
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US-10-835-096-6
Sequence 6, Application US/10835096
Sequence 6, Publication No. US20050032139A1
GENERAL INFORMATION:
APPLICANT: Heaskani, Sarkiz D.
APPLICANT: Sheung, Julie
APPLICANT: Sheung, Julie
APPLICANT: Rray, Todd R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 100.0
Matches 108; Conservative
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FEATURE:
                         LENGTH: 108
TYPE: PRT
CRGANISM: Homo sapiens
US-10-152-156-6
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SEQ ID NO 6
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APPLICANT: BROWN: Janing
APPLICANT: BROWN: Janing
APPLICANT: Sheung, Julie
APPLICANT: Sheung, Julie
APPLICANT: Sheung, Julie
APPLICANT: Sheung, Julie
TITLE OF INVENTION: ASSAYS FOR IDENTIFYING UBIQUITIN AGENTS
TITLE OF INVENTION: ASSAYS FOR IDENTIFYING UBIQUITIN AGENTS
TITLE OF INVENTION: MODIFY THE ACTIVITY OF UBIQUITIN AGENTS
FILE REFRENCE: A-66613-5/RMS/DCF
CURRENT APPLICATION NUMBER: US 09/542,497
FRIOR APPLICATION NUMBER: US 09/826,312
PRIOR APPLICATION NUMBER: US 10/091,139
PRIOR APPLICATION NUMBER: US 10/091,139
PRIOR APPLICATION NUMBER: US 10/091,139
PRIOR PILLING DATE: 2002-03-04
NUMBER OF SEQ ID NOS: 27
SOFTWARE: Patentin Version 3.1
SEQ ID NO 6: SEQ ID NOS: 27
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Best Local Similarity 100.0%; Pred. No. 7.7e-60;
Matches 108; Conservative 0; Mismatches 0; Indels 0
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                                                                                                              Sequence 6, Application US/10108767
Publication No. US20030104474A1
GENERAL INFORMATION:
APPLICANT: ISSAKAI, Sarkiz D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Homo sapiens
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RESULT 9
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FILE REPERBURC: 021044-004600US
CURRENT APPLICATION NUMBER: US/10/913,937
CURRENT FILING DATE: 2004-08-05
FRIOR APPLICATION NUMBER: US/09/914,324
PRIOR PRILING DATE: 2001-08-22
PRIOR PILING DATE: 1999-02-26
PRIOR APPLICATION NUMBER: WG 60/121,787
PRIOR PILING DATE: 1999-02-25
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PRECENTIN VOICE: 2000-02-25
NUMBER OF SEQ ID NOS: 12
SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
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                                                                                                                                                                                                                                                                                                                                                                            Query Match 100.0%; Score 616; DB 17; Length 108; Best Local Similarity 100.0%; Pred. No. 7.7e-60; Matches 108; Conservative 0; Mismatches 0; Indels 0.
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US-10-913-937-6
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Pred. No. 8.1e-51;
4; Mismatches 4; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Conaway, Joan A.
APPLICANT: Conaway, Ronald C.
APPLICANT: Takumi
APPLICANT: Oklamoma Medical Research Foundation
FILE REFERENCE: 021044-007010US
CURRENT APPLICATION NUMBER: US/10/835,096
CURRENT FILING DATE: 2004-04-28
FRIOR FILING DATE: 2001-04-03
FRIOR FILING DATE: 2001-04-03
FRIOR PILING DATE: 2001-04-03
FRIOR FILING DATE: 2001-04-03
NUMBER: OF SEQ ID NOS: 21
SEQ ID NO 6
                                                                                                                                                                                                                                                                                     ; PEATURE:
; OTHER INFORMATION: RING finger protein ROCI
US-10-835-096-6
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ORGANISM: Drosophila melanogaster
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Best Local Similarity 87.2%;
Matches 95; Conservative
                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                         LENGTH: 108
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Sequence 148916, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Town Vibus
APPLICANT: Town Vibus
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPERENCE: 38-21(5223)8
CURRENT PLILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NOS: 285684
Sequence 43736, Application US/10767701
Publication No. US20040172684A1
GENERAL INFORMATION:
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Cor, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
TITLE OF INVENTION: NUMBER: US/10/767,701
CURRENT APPLICATION NUMBER: US/10/767,701
CURRENT FILING DATE: 2004-01-29
NUMBER OF SEQ ID NOS: 63128
SEQ ID NO 47336
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 124;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          85.1%; Score 524; DB 16; Length 1
90.9%; Pred. No. 1.2e-49;
tive 2; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: Clone ID: LIBSO52-011-A1-XP1-A5.pep
US-10-767-701-43736
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Best Local Similarity 90.97
....hes 90; Conservative
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Matches 94; Conservative
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ORGANISM: Glycine max
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Query Match
Best Local Similarity 80.03
Matches 92; Conservative
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Sequence 201494, Application US/10425115
Publication No. US20040214272A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: La Royalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Con Vihua
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(5322)8
CURRENT PAPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
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Sequence 43735

Sequence 43735

Sequence 43735

Publication No. US20040172684A1

Publication No. US20040172684A1

GENERAL INFORMATION:

APPLICANT: Kovalic, David K.

APPLICANT: Zhou, Yihua

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement

FILE REFERENCE: 38-21(53535) B

CURRENT APPLICATION NUMBER: US/10/767,701

CURRENT FILING DATE: 2004-01-29

NUMBER OF SEQ ID NOS: 63128
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Pred. No. 2.2e-48;
4; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 109;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9; Indels
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US-10-767-701-43735
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US-10-425-115-201494
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
83.1%; Score 512; DB 16;
Best Local Similarity 85.6%; Pred. No. 2.1e-48;
Matches 89; Conservative 4; Mismatches 9;
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US-10-424-599-221431
'Sequence 221431, Application US/10424599
'Publication No. US20040031072A1
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1 Similarity 91.7%;
88; Conservative 4
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Best Local Simílarity
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                                                                                                                                                                                                                                                                                                                     SEQ ID NO 201494
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APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: Expensive to the control of t
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APPLICANT: Conaway, Joan A.
APPLICANT: Conaway, Joan A.
APPLICANT: Conaway, Ronald C.
APPLICANT: Conaway, Ronald C.
APPLICANT: Conaway, Takumi
APPLICANT: Conaway, Takumi
APPLICANT: Conaway, Takumi
APPLICANT: Conglex and Scr Ubiquitin Ligase
TITLE OF INVENTION: Complex and SCF Ubiquitin Ligase
TITLE OF INVENTION: Complex and SCF Ubiquitin Ligase
FILE REFERENCE: 021044-004660US
CURRENT APPLICATION NUMBER: US/10/913,937
CURRENT APPLICATION NUMBER: US/09/914,324
PRIOR FILING DATE: 2001-08-22
PRIOR FILING DATE: 2001-08-22
PRIOR FILING DATE: 1999-02-26
PRIOR FILING DATE: 1999-02-26
PRIOR APPLICATION NUMBER: WO PCT/US00/04838
PRIOR FILING DATE: 1000-02-25
NUMBER OF SEO ID NOS: 12
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 7
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80.0%; Score 493; DB 17; Length 1
Best Local Similarity 79.3%; Pred. No. 2.7e-46;
Matches 88; Conservative 5; Mismatches 14; Indels
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80.0%; Pred. No. 1.2e-47;
iive 4; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: Clone ID: PAT_MRT3847_41982C.1.pep
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Publication No. US20050019813A1
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ORGANISM: Caenorhabditis elegans
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Search completed: June 23, 2005, 15:43:29 Job time : 160 secs
70 LDNSEWEFQKYGH 82
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                                           Sequence 148915, Application US/10424599

Fublication No. US20040031072A1

GENERAL INFORMATION:

APPLICANT: La Rosa Thomas J

APPLICANT: Low Yihua

APPLICANT: Zhou Yihua

APPLICANT: Cao Yongwei

TITLE OF INVENTION: Plantes and Uses Thereof for Plant Improvement

TITLE OF INVENTION: 138-21 (53223) B

CURRENT APPLICATION NUMBER: US/10/424,599

CURRENT PILING DATE: 2003-04-28

SEQ ID NO 148915

LEMBET OF SEC ID NOS: 285684

SEQ ID NO 148915
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Publication No. US20040214272A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Zhou, Yihua
APPLICANT: Chou, Yihua
APPLICANT: No.eic Acid Molecules and Other Molecules Associated With
FILE OF INVENTION: Plants
FILE OF INVENTION WUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
SEQ ID NO 191492
LENGTH: 82
LENGTH: 82
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10 DIVVDNCAICRNHIMDLCIECQANQASATSEECTVAWGVCNHAFHFHCISRWLKTRQVCP 69
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 68.3%; Score 420.5; DB 15; Length 106; Best Local Similarity 69.2%; Pred. No. 2.4e-38; Matches 81; Conservative 5; Mismatches 8; Indels 23;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; OTHER INFORMATION: Clone ID: PAT_MRT3847_105493C.1.pep
US-10-424-599-148915
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US-10-425-115-191492
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OTHER INFORMATION: unsure at all Xaa locations
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ORGANISM: Glycine max
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ORGANISM: Zea mays
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US-10-425-115-191492
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US-10-425-115-291051

Sequence 291051, Application US/10425115

Publication No. US20040214272A1

Sequence 291051, Application US/10425115

Publication No. US20040214272A1

APPLICANT: La Rosa, Thomas J.

APPLICANT: APPLICANT: Acouption of the molecules and Other Molecules Associated With TILLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With TILLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With TILLE OF INVENTION: NUMBER: US/10/425,115

CURRENT APPLICATION NUMBER: US/10/425,115

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 369326

SEQ ID NO 291051

LENGTH: 97
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 68.2%; Score 420; DB 16; Length 97; Best Local Similarity 80.9%; Pred. No. 2.5e-38; Matches 72; Conservative 7; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: Clone ID: MRT4577_28527C.1.pep
US-10-425-115-291051
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Zea mays
FEATURE:
NAME/KEY: unsure
LOCATION: (1)..(97)
OTHER INFORMATION: unsure at all Xaa locations
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96 LDNREWEFOKYGH 108
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A;Reference number: Z17665
A;Accession: T1338
A;Actual preliminary; translated from GB/EMBL/DDBJ
A;Returns: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-136 cCAT>
A;Cross-references: UNIPROT:Q9W5E1; EMBL:AL031581; PIDN:CAA20888.1
C;Genetics:
A;Cross-references: PlyBase:PBGN0020381
A;Introns: 64/1
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A;Note: EG:115C2.11
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RING-H2 finger pro
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                                                                                                                                                                                                                                                                           1 MAAAMDVDTPSGTNSGAGKK......KTRQVCPLDNREWEFQKYGH 108
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                                            - protein search, using sw model
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T13388
T47341
T47341
T38310
S66830
T18620
T28620
T28620
T21862
S52511
G90113
T020241
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Gapop 10.0 , Gapext 0.5
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seq length: 200000000
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616
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Match Length DB
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1: pir1:*
2: pir2:*
3: pir3:*
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Perfect score:
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Maximum DB E
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91.5 14.9 496 2 B96674 91.5 14.9 571 2 T40911 90.5 14.7 677 2 T39713 90.1 14.8 530 2 T40465 90.5 14.7 677 2 T39713 90 14.6 513 2 T40465 90.1 14.6 513 2 T05877 90 14.6 513 2 T05877 90 14.6 520 2 T05878 89.5 14.4 357 2 E85592 89.5 14.4 357 2 E85592 88.5 14.4 357 2 E85592 88.5 14.4 524 2 F96572 88.5 14.4 524 2 F96572 88.5 14.4 524 2 F96572 88.1 14.3 101 2 S15788 88.1 14.3 101 2 S1578 88.2 14.4 524 2 F96572 88.3 14.4 524 2 F96572 88.8 14.3 101 2 S1578 88.1 14.3 100 0\$; Pred bes preliminary; translated from cule type: mkNA dues: 1-108 «KAA» cule type: mkNA 1 MAAAMDVDPSGTNSGAGKKRFEVK	hypothetical prote probable PHD-type ORF MSV205 tryptop zinc finger protei hypothetical prote related to COP1-in hypothetical prote probable RING zinc hypothetical prote hypothetical prote probable RING zinc protein F12M16.10 intermediate early protein ZK637.14 [RING-H2 finger pro	GNMENTS 28-Jul-2000 #text_change 09-Jul-2004 ; Skowyra, D.; Moreland, R.J.; Iliopoulos, O.; Lar umor suppressor complex and SCF ubiquitin ligase. 20; PMID:10213691 GB/EMBL/DDBJ L:AF140598; PIDN:AAD29715.1	2; Length 108; -59; 0; Indels 0; Gaps 0; ILVVDNCAICRNHIMDLCIECQANQ 60	nila melanogaster)) #text_change 09-Jul-2004 rson, N.; Campbell, L.; Glover, D. of Drosophila melanogaster.
30 91.5 14.9 496 2 31 91.5 14.9 571 2 33 90.5 14.7 677 2 34 90.5 14.7 677 2 35 90.14.6 5213 2 36 90.14.6 5213 2 37 89.5 14.5 502 2 38 99.14.4 357 2 41 88.5 14.4 357 2 42 88.5 14.4 357 2 42 88.5 14.4 357 2 43 88 14.3 141 2 44 88.5 14.4 524 2 45 88.5 14.4 524 2 46 88.5 14.4 357 2 47 88.5 14.4 357 2 48 81 14.3 161 2 48 81 14.3 161 2 48 81 14.3 161 2 48 81 14.3 161 2 48 81 14.3 161 2 48 81 14.3 161 2 48 81 14.3 161 2 48 81 14.3 161 2 48 81 14.3 100 2 48 14.4 357 2 48 81 14.3 161 2 48 81 14.3 161 2 48 81 14.3 100 2 48 14.4 357 2 48 81 14.3 161 2 48 81 14.3 161 2 48 81 14.3 100 2 48 81 14.3 100 2 48 81 14.3 100 3 40 10 10 3 40 10 10 3 40 10 10 3 40 10 10 3 40 10 10 3 40 10 10 3 40 10	B96674 B96674 T289511 T14811 T14811 T05977 T05621 T016621 T19377 T19377 T19377 T19377 T19377 T19377 T19377 T19377	ALIGNMENTS human vision 28-Jul-200 d, M.N.; Skowyra, e VHL tumor suppr :99234320; PMID:11 d from GB/EMBL/DDI	; Score 616; DB ; Pred. No. 9.9e. 0; Mismatches KKRFEVKKWNAVALWAWI	fruit fly (Drosop) er vision 13-Aug-1999 mitsou, A.; Hende: ry, May 1999 stal X chromosome
30 91.5 14.9 496 32 31 91.5 14.9 571 33 90.5 14.9 571 34 90 14.6 5213 35 90.14.6 5203 36 89.5 14.7 677 39 89.5 14.5 524 40 88.5 14.4 456 41 88.5 14.4 357 42 88.5 14.4 524 43 88.5 14.4 524 44 88.5 14.4 524 45 88.5 14.4 524 46 88.5 14.4 524 47 88.5 14.4 524 48 81.5 14.7 524 48 81.5 14.7 524 48 81.5 14.7 524 48 81.5 14.7 524 48 81.5 14.4 524 48 81.5 14.4 524 48 81.5 14.4 524 48 81.5 14.4 524 48 81.5 14.4 524 48 81.5 14.7 524 48 81.5 14.4 524 48 81.5 14.4 524 48 81.5 14.4 524 48 81.5 14.4 524 48 81.5 14.4 524 48 81.5 14.4 524 48 81.5 14.4 524 48 81.5 14.4 524 48 81.5 14.4 524 48 81.5 14.4 524 524 524 524 5254 5254 5254 5254 52			O. O#	l - Jast Lre rrla
30 91.5 14.9 31 91.5 14.9 32 91.5 14.9 33 90.5 14.7 34 90 14.6 36 90 14.6 38 90.5 14.5 39 89.5 14.5 39 89.5 14.4 41 88.5 14.4 42 88.5 14.4 42 88.5 14.4 43 88 14.3 44 88.5 14.4 45 88 14.3 45 88 14.3 46 88 14.3 47 88 14.3 48 88.5 14.4 48 88.5 14.4 49 88.5 14.4 40 88 14.3 42 88 14.3 44 88.5 14.4 42 88.5 14.4 43 88 14.3 45 88 14.3 46 88 14.3 47 88 14.3 48 88 14.3 4	496 531 532 1208 1208 6242 6242 456 1316 1111	ported) 8 (man) 8 (man) 1. (A., Cc.M., Cc.M.	1000 rvative IPSGTNE TVAWGVC	15C2.11 melanoc equence P.; De Data Ling the
30 91.5 31 91.5 32 91.5 33 90.5 34 90.5 35 90.5 36 89.5 40 88.5 41 88.5 42 88.5 43 88.5 44 88.5 44 88.5 45 88.5 46 88.5 47 88.5 48 88.5 48 88.5 48 88.5 48 88.5 48 88.5 49 88.5 40 88.5 41 88.5 42 88.5 44 88.5 45 88.5 46 5 47 1111 1 11146 Accession: TS Status: prelim Accession: TS Accession: TS Accession: TS Accession: TS	0.0866000000000000000000000000000000000	n 1 [im 2000 #5 1146 2000 #5 1146 2009, D 2009, D 3 compo ber: 22 1146 1146 1146 1146 1146 1146	nilarit Conse AAAMDVD AAAMDVD SATSEEC	otein 1 ophila 1999 #8 3388 alenti, ae EMBL
30 31 32 32 33 33 33 33 33 33 33 33 33 33 33	999 888 889 999 999 999 899 899 999 999	c protein 28: Houler 28: Juler 3ion: TS: 3, T.; K 4, T.; K 7: Rbx1, 5 8bx1, 6 3ion: TS: 3: prelii 11e type 11e type 11e type 11e type 11e type 12es: 1-1.	atch cal S 108 1 1 61 61	ical presses Droses Droses Droses Droses Droses 13-Aug-sion: Tl. 3, C.; V. 3, C.; V. 5d to the lottion:
SERVICIONIES B & B & PORTE B B & B & B & B & B & B & B & B & B &	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	RESULT 1 T51146 ring-box C;Species C;Accessi R;Kamura, SA;Tille: A;Referen A;Referen A;Referen A;Referen A;Referen C;Genetic C;Genetic A;Genetic A;Genetic	Query Best Match	T113388 hypothet C,Specie C,Date: C,Access R;Salles Submitte A,Descri

82.8%; Score 510; DB 2; Length 136;

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A;Accession: S66830
A;Molecule type: DNA
A;Residues: 1-121 <ARI
A;Csss-references: UNIPROT:Q08273; EMBL:Z74876; NID:g1420022; PID:g1420024; MIPS:YOL133v
A;Experimental source: strain S288C
B;Ajddea, M.; Piedrafita, L.; Casas, C.; Casamayor, A.; Khalid, H.; Balcells, L.; Arino, C; Rast 12, 1053-1058, 1996
A;Title: Sequence analysis of a 12 801 bp fragment of the left arm of yeast chromosome Xi
Protein and six other open reading frames.
A;Reference number: S72030; MUD:97051593; PMID:8896270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hypothetical protein YOL133w - yeast (Saccharomyces cerevisiae)
N,Alternate names: hypothetical protein AOAA121; hypothetical protein 00511
S,Species: Saccharomyces cerevisiae
C,Species: 12-Jul-1996 #sequence_revision
C,Accession: S66830; S72035
C,Accession: S66830; S72035
S,Azino, J; Casamayor, A.; Gamo, F.J.; Gancedo, C.; Lafuente, M.J.; Aldea, M.; Casas, submitted to the Protein Sequence Database, July 1996
A,Reference number: S66814
                                                                                                                                              1 MAQASDSTAMEVEEATNQTV-KKRFVKKWSAVALWAWDIQVDNCAICRNHIMDLCIBCQ 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21 RFEVKKWNAVALWAWDIVVDNCAICRNHIMDLCIECQANQASATSEECTVAWGVCNHAFH 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20 RFEIKKWNAVALWQWDIVVDNCAICRNHIMDLCIECQANTDSAAAQECTVAWGTCNHAFH 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-121 (ALD)
A;Cross-references: EMBL:X95465; NID:g1628437; PIDN:CAA64737.1; PID:g1628443
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, DNA
C;Genetics:
A;Gene: SGD:HRT1
                                                                                                                                                                                                                                                                                                                                                                                                            C;Species: Schizosaccharomyces pombe
C;Species: Schizosaccharomyces pombe
C;Species: Schizosaccharomyces pombe
C;Dacesion: T38310
C;Accession: T38310
R;Brown, D.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Wood, V. submitted to the EMBL Data Library, September 1997
                                                                                                        1 MAAAMD----VDTPSGTNSGAGKKRFEVKKWNAVALWAWDIVVDNCAICRNHIMDLCIECQ
                                                       4; Gaps
                                                                                                                                                                                                                                                 60 ANQAAGLKDECTVAWGNCNHAFHFHCISRWLKTRQVCPLDNREWEFQKYGH 110
                                                                                                                                                                                                                       58 ANQASATSEECTVAWGVCNHAFHFHCISRWLKTRQVCPLDNREWEFQKYGH 108
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79.3%; Pred. No. 1.4e-45;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
76.1%; Score 469; DB 2;
Best Local Similarity 87.5%; Pred. No. 5e-43;
Matches 77; Conservative 4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        81 FHCISRWLKTRQVCPLDNREWEFQKYGH 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         80 FHCISRWLNTRNVCPLDNREWEFQRYGH 107
                          Best Local Similarity 79.3% Matches 88; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Map position: 1
A; Introns: 25/3; 75/3; 106/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Reference number: Z21733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A, Gene: SPDB:SPAC23H4.18c
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                                                                                                                                                                                                                                                                                                                                                                                                T38310
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Submitted to the EMBL Data Library, April 1996

A; Reference number: Z20425

A; Status: preliminary; translated from GB/EMBL/DDBJ

A; Status: preliminary; translated from GB/EMBL/DDBJ

A; Rolecule: Lype: DNA

A; Residues: 1-110 < WIL>
A; Cross-references: UNIPROT: Q23457; EMBL: Z70757; PIDN: CAA94801.1; GSPDB: GN00023; CESP: ZR

A; Experimental source: clone ZK287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N;Alternate names: protein T21C14.50
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004
C;Accession: T47341
R;Delseny, M.; Berger, C.; Cooke, R.; Gaubier, P.; Grellet, F.; Laudie, M.; Mewes, H.W.;
                                                                                                                                                                                                                                                          60 LWAWDIVVDNCAICRNHIMDLCIECOANOASATSEECTVAWGVCNHAFHFHCISRWLKTR 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MAAAMDVDTPSGTNSGAGKKRFEVKKWNAVALWAWDIVVDNCAICRNHIMDLCIECQANQ 60
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                                                                                                              -----WNAVA 31
                                                                                                                                                                1 MEVDEDGYEVPSSSSKG-DKKRFEVKKVSGQQKSRVIVNECTDGNTSSFPLRRKQWNAVA 59
                                                                                                                                                                                                                          32 LWAWDIVVDNCAICRNHIMDLCIECQANQASATSEECTVAWGVCNHAFHFHCISRWLKTR 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hypothetical protein ZK287.5 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15. Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T27823
                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A,Map position: 3
A,Introns: 43/1; 60/1; 80/1; 104/1
A,Introns: T21C14.50
C,Superfamily: yeast hypothetical protein YOL133w; RING finger homology
                                                       34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 ASATSEECTVAWGVCNHAFHFHCISRWLKTRQVCPLDNREWEFQKYGH 108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ch 81.0%; Score 499; DB 2; Length 115; I Similarity 81.5%; Pred. No. 3.3c-46; 88; Conservative 5; Mismatches 13; Indels
                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: UNIPROT:Q9M2B0; EMBL:AL138639
A;Experimental source: cultivar Columbia; BAC clone T21C14
C;Genetics:
. 2.6e-47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              submitted to the Protein Sequence Database, April 2000
A;Reference number: Z24462
A;Accession: T47341
                          Pred. No. 2.6e
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ring-box protein-like - Arabidopsis thaliana
                                                                                                              5 MDVD-----TPSGTNSGAGKKRFEVKK-
                                                                                                                                                                                                                                                                                                                                                                      120 QVCPLDNREWDFQKYGH 136
                                                                                                                                                                                                                                                                                                                                      92 OVCPLDNREWEFOKYGH 108
                          Best Local Similarity 69.3%;
Matches 95; Conservative
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Best Local Similarity
Matches 88; Conserval
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: DNA
A; Residues: 1-115 <DEL>
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A;Map position: 5
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Query Match

Best Local Matches 6

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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Mosediduss: 1.135 CMIL>
A;Crose-references: UNIENOT:020052; EMBL:Z46242; PIDN:CAA86328.1; GSPDB:GN00021; CESP:F3:
A;Experimental source: clone F35G12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: UNIPROT:09UT86; EMBL:AL109739; NID:e1534774; PIDN:CAB52266.1; GSPDB:CA;Experimental source: strain 972h-; cosmid c343
                                                                                                                               1 MINSSNADSQEGSTSAQKQKTANPSESRPFVLKKWNALAVWAWDVECDTCALCRVHLMEE 60
                                                                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein SPAC343.03 - fission yeast (Schizosaccharomyces pombe) C;Species: Schizosaccharomyces pombe C;Species: O3-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T21802
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                                                                                              1 MAAAMDVDTPSGTNSGAGKKR-----FEVKKWNAVALWAWDIVVDNCAICRNHIMDL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21 RFEVKKWNAVALWAWDIVVDN-CAICRNHIMDLCIECQANQASATSEECTVAWGVCNHAP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 23.8%; Score 146.5; DB 2; Length 135; Best Local Similarity 33.3%; Pred. No. 1.8e-08; Matches 28; Conservative. 10; Mismatches 35; Indels 11;
                                12;
                                                                                                                                                                                                                                                        53 CIECQANQASATSEECTVAWGVCNHAFHFHCISRWLKTRQVCPLDNREW 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Accession: T38652
R;Murphy, L.; Harris, D.; Wood, V.; Rajandream, M.A.; Barrell, B.G.
submitted to the EMBL Data Library, August 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 33.7%; Pred. No. 1.5e-10;
Matches 28; Conservative 16; Mismatches 30; Indels
   Best Local Similarity 41.3%; Pred. No. 2.5e-21;
Matches 45; Conservative 20; Mismatches 32; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Reference number: 221804
A;Reference number: 221804
A;Accession: T38652
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-94 <MUR>
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A;Reference number: Z19473
A;Accession: T21802
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Gene: SPDB: SPAC343.03
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A; Introns: 7/1; 48/1
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A;Experimental source: strain Bristol N2; clone R10A10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ----NQASATSEECTVAWG 73
                                                                                                                                                                                                                                                                                      5 MDVDTPSGTNSGAG-----KKRFEVKKWNAVALWAWDIVVDNCAICRNHIMDLCI 54
                                                                                                                                                                                                                                                                                                                       8 MDVDEDESQNIAQSSNQSAPVETKKKRFEIKKWTAVAFWSWDIAVDNCAICRNHIMEPCI 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             nypothetical protein C0845c - malaria parasite (Plasmodium falciparum)
s;Species: Plasmodium falciparum
s;Species: Plasmodium falciparum
s;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hypothetical protein R10A10.2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                           Gaps
A,Cross-references: SGD:S0005493
A,Map position: 15L
A,Note: Yold:33w
C,Superfamily: yeast hypothetical protein YOL133w; RING finger homology
                                                                                                                                                                                                                                                                                                                                                                                                            C; Superfamily: yeast hypothetical protein YOL133w; RING finger homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 61.4%; Score 378; DB 2; Length 166; Best Local Similarity 69.6%; Pred. No. 4e-33; Matches 64; Conservative 5; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A, Cross-references: UNIPROT:077367; EMBL:298551; PIDN:CAB11123.2
                                                                                                                                                      62.5%; Score 385; DB 2; Length 121;
56.6%; Pred. No. 5.3e-34;
ive 10; Mismatches 29; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 2; Length 112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Accession: T29620
R;Wamsley, P.; Bradshaw, H.
submitted to the EMBL Data Library, November 1996
A;Description: The sequence of C. elegans cosmid R10AlO.
A;Reference number: 220653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22 FEVKKWNAVALWAWDIVVDNCAICRNHIMDLCIECQA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Status: preliminary; translated from GB/EMBL/DDBJ
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Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   74 VCNHAFHFHCISRWLKTRQVCPLDNREWEFQK 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R;Lawson, D.; Bowman, S.; Barrell, B.
submitted to the EMBL Data Library, August 1997
A;Reference number: Z18935
A;Accession: T18513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 266;
                                                                                                                                                                                                                        64; Conservative
                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Molecule type: DNA
Residues: 1-166 <LAW>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Residues: 1-112 <WAM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A,Gene: CESP:R10A10.2
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A:Introns: 17/2; 59/1
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A;Map position: 3 A;Introns: 19/1 A; Note: C0845c

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Query Match

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A;Residues: 1-2160 <WIL>
A;Cross-references: UNIPROT:017709; EMBL:275533; PIDN:CAA99823.1; GSPDB:GN00019; CESP:H06
A;Experimental source: clone C5464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein T17F15.100 - Arabidopsis thaliana ($\text{C}$)$ pecies: Arabidopsis thaliana ($\text{mouse-ear}$ cress)
$C$$ pate: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
$C$$ Accession: T06600
$R$$ Quetier, $F$$; Choisne, $N$$, Robert, $C$$; Brottier, $P$$ Wincker, $P$$; Cattolico, $L$$, Artigue submitted to the Protein Sequence Database, April 1999
$A$$ Reference number: $Z$$793
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Introns: 49/3; 130/3; 190/3; 237/3; 290/1; 463/3; 507/1; 524/2; 545/1; 636/2; 663/2; 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Accession: T06680
A;Molecule type: DNA
A;Residues: 1-349 <QUE>
A;Cross-references: UNIPROT;Q9SU66; EMBL:AL049658; GSPDB:GN00061; ATSP:T17F15.100
A;Experimental source: cultivar Columbia; BAC clone T17F15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               --- 2117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Residues: 1-2160 <W12>
;Cross-references: EMBL:299772; PIDN:CAB16922.1; GSPDB:GN00019; CESP:H05L14.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        64
                                                             22 EKCAICRNNLEDNAPDFBERVGKHSKNFLDQISKNCFLAYGRCGHSFHLICIENWILLNK 81
                                                                                                                                                                                                                                                                                                                                              hypothetical protein HO5L14.2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T20241; T23049
R;Wilkinson, J.
Submitted to the EMBL Data Library, June 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8 DIPSGINSGAGKKRFEVKKWNAVALWAWDIVV---DNCAICRNHIMDLCIECQANQASAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2068 DVPMPFSETVMKKMFQCSGYELDVVTEREEVVBEBDGCLIC-TEIIEEAVE---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels 17;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               / Match 18.9%; Score 116.5; DB 2; Local Similarity 30.5%; Pred. No. 0.00044; nes 29; Conservative 11; Mismatches 38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2118 ----TVTCDTCTREYHYHCISRWLKINSVCPQCSR 2148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Accession: T20241
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A,Status: preliminary, translated from GB/EMBL/DDBJ
A,Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             65 SEECTVAWGVCNHAFHFHCISRWLKTRQVCPLDNR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R;Barlow, K. substrated Library, October 1997 submitted to the EMBL Data Library, October 1997 A;Reference number: Z19662 A;Recession: T23049
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16.9%; Score 104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Map position: 3
A;Introns: 26/1; 81/2
F;203-254/Domain: RING finger homology <RRN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Experimental source: clone H05L14
                              DNCAICRNHIMDLCIECQ-
                                                                                                                                                 93 VCPLDNREWEFQ 104
                                                                                                                                                                                         82 NCPLCSRIWVYE 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Reference number: Z19241
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Gene: CESP:H05L14.2
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Best Local Si
Matches 29;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Residues: 1-165 cAND>
A;Cross-references: UNIPROT:Q12157; EMBL:Z48432; NID:g683669; PIDN:CAA88351.1; PID:g6836
A;Experimental source: strain S288C
A;Experimental source: strain S288C
B;Urreserazuu, L.A.; Andare, B.; Vissers, S.
submitted to the Protein Sequence Database, July 1996
A;Reference number: S67535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rpp1 protein (imported) - Guillardia theta nucleomorph C; Species: nucleomorph Guillardia theta C; Species: nucleomorph Guillardia theta A; Note: a nucleomorph Guillardia theta A; Note: a nucleomorph is the vestigial nucleus of a eukaryotic endosymbiont C; Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004 C; Accession: G90113
R; Douglas, S; Zauner, S; Fraunholz, M; Beaton, M; Penny, S; Deng, L.T.; Wu, X; Rei Nature 410, 1091-1096, 2001
A; Reference number: A99082; MulD:11323671; PMID:11323671
A; Accession: G90113
A; Accession: G90113
A; Residues: 1-99 < DOUS
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A;Residues: 1-165 <URR>
A;Cross-references: EMBL:274056; NID:g1430968; PIDN:CAA98564.1; PID:e252972; PID:g143096
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'n
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R,Andre, B.; Vissers, S.; Urrestarazu, L.
submitted to the EMBL Data Library, February 1995
A,Description: The sequence of a 42 kb segment located on the left arm of chromosome A;Reference number: S52492
A;Accession: S52511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ä
53 VKKLHVCGEWKWLQGGEDTCGICRMEFESAC----NMCKFPGDDCPLVLGICRHAFHRH 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----VDNCAICRNHIMDLCIECQANQAS 62
                                                                                                                                                                                                                                                                      hypothetical protein YDL008w - yeast (Saccharomyces cerevisiae)
NiAlternate names: hypothetical protein D2900
CiSpecies: Saccharomyces cerevisiae
CiSpecies: Saccharomyces cerevisiae
CiSpate: 08-May-1995 #sequence_revision 21-Jul-1995 #text_change 09-Jul-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Score 136; DB 2; Length 165; ; Pred. No. 2.8e-07; 19; Mismatches 33; Indels ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            57 FPGDQCPLVIGLCHHNFHDHCIYRWLDTPTSKGLCPMCRQTFQLQK 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          63 ATSEECTVAWGVCNHAFHFHCISRWLKT---RQVCPLDNREWEFQK 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cch 21.5%; Score 132.5; DB 2; Length al Similarity 33.3%; Pred. No. 4e-07; 24; Conservative 14; Mismatches 27; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22.1%; Score 136;
                                                                83 CISRWL----KTRQVCPLDNREW 101
                                                                                                  108 CIDKWIAAPTNQPRAQCPLCRQDW 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Experimental source: strain S288C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: SGD:S0002166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 26.4%
Matches 28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 24; Conserv
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A; Genome: nucleomorph
C; Keywords: nucleomorph
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Molecule type: DNA; Residues: 1-165 <A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Accession: S67540
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41 NCAICRNHIMDLCIECQANQASATSEECTVAWGVCNHAFHFHCISRWLKTRQVCPLDNR 99
Best Local Similarity 33.9%; Pred. No. 0.0016;
Matches 20; Conservative 8; Mismatches 17; Indels 14; Gaps
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206 DCAVCLNEFSD----
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probable RING zinc finger protein FIM20.30 [imported] - Arabidopsis thaliana C; Species: Arabidopsis thaliana (mouse-ear cress)
C; Species: Arabidopsis thaliana (mouse-ear cress)
C; Date: 02-Nar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C; Accession: C96775
R; Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A; Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.; Southwick, A.M.; Sun, H.; Tallon, A; Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A; Reference number: A86141; MUID:21016719; PMID:11130712
A; Reference number: A86141; MUID:21016719; PMID:11130712
A; Residues: 1-249 <STO>
A; References: UNIPROT: Q9CA55; GB: ABOOS173; NID:g6539262; PIDN:AAF15932.1; GSPDB:GN

A;Gene: F1M20.30 A;Map position: 1

Gaps 16.6%; Score 102.5; DB 2; Length 249; 26.0%; Pred. No. 0.0016; tive 22; Mismatches 38; Indels 17; Query Match Best Local Similarity 26.0% Matches 27; Conservative

5 MDVDTPSGTNSGAGKKRFEVKKMNAVALW-----AMDIVVDNCAICRNHI------MDL 52

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53 CIECQANQASATSEECTVAWGVCNHAFHFHCISRWLKTRQVCPL 96

Search completed: June 23, 2005, 15:30:28 Job time : 40 secs

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Protein Sequence Searches - February 2005

All of the sequence databases on ABSS have recently been updated.

- permanent accession numbers. The new UniProt record may not contain the previous temporary numbers from the most recent version of UniProt. These sequences have been assigned new Please note that the curators of the UniProt database have purged some temporary accession accession number.
- extension .rup) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein If you encounter an accession number from an older search run against UniProt (results file Archive database (UniPARC) at:

http://www.pir.uniprot.org/database/archive.shtml

If you have any questions regarding this information or your results, please contact any STIC searcher.

members of the public who may encounter UniProt temporary accession When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or numbers.

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Best Available Copy

GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

June 23, 2005, 15:18:51; Search time 176 Seconds (without alignments) 314.230 Million cell updates/sec Run on:

Title: Perfect score: Sequence:

US-09-541-462B-2 616 1 MAAAMDVDTPSGTNSGAGKK......KTRQVCPLDNREWEFQKYGH 108

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1612378 seqs, 512079187 residues Searched:

1612378 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	SUMMARIES	Description	HUMAN P62877 homo sapien	mus n		0642 j 6		07q9j7		Q88380 oryza sativ		Q7y042		07sbt1		Q23457	RBX1_SCHPO 013959 schizosacch		Q6bkz3 debaryomyce	66e59Ö								MOUSE Q9wtz1 mus musculu	Q9v607 drosophila	Q7pnw0 anopheles		P91404 caenorhabdi	
		DB	-	~	~	~	-	~	-	~	N	7	-	7	-	-	-	-	~	~	-	~	~	~	~	N	-	Н	~	N	~	~	
		Length	108	108	108	111	108	174	108	114	123	110	118	116	115	110	107	122	115	186	121	108	107	107	110	92	113	113	113	109	96	112	
		ያኗ	100.0	100.0	100.0	98.2	98.		98	85	85.0	84.9	83.5	82.0	81.0	80.0	76.1	65.0	64.9	64.8	62.5	62.3	62.2	61.4	9.95	50.0	47.4	47.2	46.2	46.1		43.2	
Match Length 100.0		Scor	:	919	616	605	604	539.5	534	523.5	523.5	523	514.5	505	499	493	469	400.5	400	399	385	384	383	m	m	308	292	290.5	284.5	284	281.5	266	
Match Length 100.0		Result No.	1	7	m	4	Z,	9	7	œ	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23		25		27	28	29	30	

O9cpx9 mus musculu O9nyg5 homo sapien O7q443 anopheles g Q8100 cryza sariv Q7k43 drosophila O7qx96 giardia lam Q6-163 yarrowia li Q9ut86 schizoacch O7rga3 plasmodium Q6-169 p
AN11_MOUSE AN11_HUMAN QYQ443 QYQ443 QYQ443 QYQX36 QYQX36 QYQX36 QYGCLE3 YF93 XF93 SCHPO QYRGA3 QCCUO QYRGA20 QYRGA20 QYRGA20 QYRGA20 QYRGA20 QYRGA20 QYRGA20 QYRGA20
44000000000000
884 884 109 109 866 866 1135 1135 149
223.9 223.9 223.9 223.9 223.9 223.9
209 202.5 202.5 198 197 169.5 164.5 151 146.5 147
W W W W W W W W W W W W W W W W W W W

ALIGNMENTS

As Laired G.K., Langford C.F., Lavaredha W.A., Lloyd C., Lloyd D.W.,
A. Maritra J. M., Parler B., Pearce A.V., Pearson D. Phillings B. J.,
A. Godell C.W., Fayler B., Pearce A.V., Pearson D. Phillings B. J.,
A. Godell C.W., Payler B., Pearce A.V., Sanal D. B.,
A. Godell C.W., Payler B.,
A. Godell C.W., Struck C.D., Small D. S., Smith M.L.,
A. Mandin M. Wall M. Walls W. Wall M. Wall W. Wal

Nature 416:703-709(2002).

CEC(VHL) (CUL2-elonging BC-VHL) E3 ubiquitin ligase complexes, which mediate the ubiquitination and subsequent proceasomal degradation of target proteins involved in cell cycle progression, signal transduction and transcription. Through the RING-type zinc finger, seems to recruit the E2 ubiquitination enzyme, like CDC34, to the complex and brings it into close proximity to the substrate. Probably also stimulates CDC34 autoubiquitination. Promotes the neddylation of CUL1 and probably CUL2.

Promotes the neddylation of CUL1 and probably CUL2.

Promotes the neddylation of third step.

Promotes the neddylation of CUL1 and probably CUL2.

COMPLEXED TO CUL2 or CUL2 and PLESS.

COMPLEXED TO CUL2 and NEDS: consisting of CUL1, RBX1, SKP1 and FBXM9. Part of a SCF-like complexes with elongin BC complex (TCEB1 and TCEB2), CUL2 or CUL2 and MDY1. Part of multisubunit complexes with elongin BC complex (TCEB1 and TCEB2), CUL2 and MDY1. Part of multisubunit complexes with elongin BC complex (TCEB1 and TCEB2), elongin A/TCEB3 or SOCS1 or WSB1 and CUL3.

CULAA, CULAB, CUL3 and CUL7. Probably also with CUL2, CUL3, CUL3, and CUL4, Part of MULT. Part of MULT. Part of MULT. Part of MULT. CUL3. IDENTIFICATION IN E3 UBIQUITIN LIGASE COMPLEX WITH MUF1, AND IDENTIFICATION IN COMPLEXES WITH CUL5.
MEDLINE=1380117; PubMed=11384984; DOI-10.1074/jbc.M103093200;
MEDLINE=21380117; Divended: 1.0. Schmidt S.L., Lane W.S., Querido E., Branton P.E., Shilatifard A., Conaway R.C., Conaway J.W.;
Muf1, a novel elongin BC-interacting leucine-rich repeat protein that can assemble with Cul5 and Rbx1 to reconstitute a ubiquitin ligase.";
J. Biol. Chem. 276:29748-29753(2001). DEDITIFICATION IN E3 UBIQUITIN LICASE COMPLEX WITH MEDB.
MEDLINE=22155962; PubMed=12149480; DOI=10.1073/pnas.162424199;
Brower C.S., Sato S., Tomomori.Sato C., Kamura T., Pause A.,
Stearman R., Klausner R.D., Malik S., Lane W.S., Sorokina I.,
Roder R.G., Conaway J.W., Conaway R.C.;
"Mammalian mediator subunit mMEDB is an elongin BC-interacting protein that can assemble with Cul2 and Rbx1 to reconstitute a ubiquitin X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS) OF 19-108 IN COMPLEX WITH 17-776 OF CUL1, AND X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS) IN SCF COMPLEX WITH CUL1; SKP1 AND SKP2.

MEDLINE=21959435; Pubmed=11961546; DOI=10.1038/416703a; ç Zheng N., Schulman B.A., Song L., Miller J.J., Jeffrey P.D., Wang P., Chu C., Koepp D.M., Elledge S.J., Pagano M., Conaway R.C., Conaway J.W., Harper J.W., Pavletich N.P.; "Structure of the Cull-Rbx1-Skpl-F boxSkp2 SCF ubiquitin ligase MEDLINE=20047893; PubMed=10579999; DOI=10.1101/gad.13.22.2928; Kamura T., Conrad M.N., Yan Q., Conaway R.C., Conaway J.W.; "The Rbx1 subunit of SCF and VHL B3 ubiquitin ligase activates Rub1 modification of cullins Cdc33 and Cull." MEDLINE=22388271; PubMed=12481031; DOI=10.1073/pnas.252646399; Dias D.C., Dolios G., Wang R., Pan Z.Q.; "CULT: a DOC domain-containing cullin selectively binds 5kpl.Fbx29 form an SCF-like complex."; Parce. Natl. Acad. Sci. U.S.A. 99:16601-16606(2002). MEDLINE=20481777; PubMed=11027288; DOI=10.1128/MCB.20.21.8185-8197.2000; Purukawa M., Zhang Y., McCarville J., Ohta T., Xiong Y.; Etticient "The CUll C-terminal sequence and ROC1 are required for efficient nuclear accumulation, NEDD8 modification, and ubiquitin ligase IDENTIFICATION IN SCF-LIKE COMPLEX, AND INTERACTION WITH CUL7 Proc. Natl. Acad. Sci. U.S.A. 99:10353-10358(2002). activity of CUL1."; Mol. Cell. Biol. 20:8185-8197(2000). FUNCTION, AND SUBCELLULAR LOCATION Genes Dev. 13:2928-2933(1999). complex." ligase.

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STRAIN=C57BL/6; TISSUE=Brain, and Breast tumor;
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PERGINECTOR FROM N.A.

PERGINECTOR FROM N.A.

REPLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;

REDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;

RA Nikaido I., Gaston R., Raschan H., Ranchanch C., Golobori T., Randarelli R., Haragin A., Randin A., Randin A., Randin A., Randin A., Randin A., Rawaji H., Rawasawa Y., Redzierski R.M., King B.L., Randin A., Rawaji H., Kawasawa Y., Redzierski R.M., King B.L., Randin A., Rawaji H., Marchionni L., McKenzie L., Waiki H., Rayashima T., Nummata K., Okido T., Pavan W.J., Pertea G., Peeole G., Redzierski R.M., Schneider C., Reed D.J., Reid J., Ring B.Z., Ringwald M., Sandelin A., Schneider C., Semple C.A., Sectou M., Shimada K., Shinada K., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wall R., Warner A., Schneider C., Semple C.A., Sectou M., Shinada K., Wanner A., Randin M., Sahashikawa T., Konno H., Nakamura M., Sahasaki D., Sakai K., Sakai K.,
                                                                                                                                                                            9
                                                                                                                                                                                                      1 MAAAMDVDTPSGTNSGAGKKRFEVKKWNAVALWAWDIVVDNCAICRNHIMDLCIECQANQ 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=99224320; PubMed=10213691; DOI=10.1126/science.284.5414.657; Kamura T., Koepp D.M., Conrad M.N., Skowyra D., Moreland R.J., Iliopoulos O., Lane W.S., Kaelin W.G. Jr., Elledge S.J., Conaway R.C., Harper J.W., Conaway J.W.; tumor suppressor complex and SCF ubiquitin ligase.";
                                                                                                                                                                         1 MAAAMDVDTPSGTNSGAGKKRFEVKKWNAVALWAWDIVVDNCAICRNHIMDLCIECQANQ
                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus. NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                           61 ASATSEECTVAWGVCNHAFHFHCISRWLKTRQVCPLDNREWEFQKYGH 108
                                                                                                                                                                                                                                                                                                        61 ASATSEECTVAMGVCNHAFHFHCISRWLKTRQVCPLDNREWEFQKYGH 108
                                                                          Length 108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A., AND IDENTIFICATION IN CBC (VHL) COMPLEX.
                                                                                                                           Indels
-!- SUBCELLULAR LOCATION: Cytoplasmic and nuclear.
                                                                                                                                ö
                                                                        100.0%; Score 616; DB 1;
100.0%; Pred. No. 6.6e-61;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                FRXI_MOUSE STANDARD; PRT; 108 AA. P62878; Q8N628; Q9D1S2; Q9WUK9; Q9Y254; 10-0CT-2003 (Rel. 42, Last sequence update) 25-0CT-2004 (Rel. 45, Last annotation update)
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Nature 420:563-573(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RING-box protein 1 (Rbx1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Science 284:657-661(1999).
                                                                                                                         fatches 108; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  musculus (Mouse).
                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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RBX1_MOUSE
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SEQUENCE FROM N.A.

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MEDLINE=22388257; PubMed=1247732; DoI=10.1073/pnas.242603899;
A Klausner R.L., Feingold E.A., Grouse L.H., Derge J.G.,
A Altschul S.F., Zeeberg B. Buetow K.H., Schaefer C.F., Bhat N.K.,
A Altschul S.F., Zeeberg B. Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
A Altschul S.F., Zeeberg B. Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
A Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Frange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McKwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
A Hichards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Whiting M., Madan A., Young A.C., Shevchanko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Garimwood J., Schmutz J., Myers R.M.,
Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
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MEDLINE=20106779; PubMed=10643962;
MEDLINE=20106779; PubMed=10643962;
MEGER F., Alliel P.M.;
Rieger F., Alliel P.M.;
"Genomic organization and expression of the ubiquitin-proteasome complex-associated protein Rbx1/ROC1/Hrtl.";
"Gell. Mol. Biol. 45:1131-1137(1999).
Cell. Mol. Biol. Advisor Biol. Bi
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-!- PATHWAY: Ubiquitin conjugation; third step.
-!- PATHWAY: Ubiquitin conjugation; third step.
-!- SUBUNIT: Part of a SCF complex consisting of CUL1, RBX1, SKP1 and SKP2. Part of a SCF-like complex consisting of CUL7, RBX1, SKP1 and FBXW8. Part of CBC(VHL) complexes with elongin BC complex (TCEB1 and TCEB2), CUL2 or CUL5 and WHI. Part of multisubunit B3 ubiquitin ligase complexes with elongin C complex (TCEB1 and TCEB2), CUL5 and MEDS; elongin BC complex (TCEB1 and TCEB2), CUL5 and MUFI. Part of multisubunit complexes with elongin BC complex (TCEB1 and TCEB2), alongin ACTEB3 or SOCSI or WSB1 and CUL5.

INCEB1 and TCEB2), alongin A/TCB3 or SOCSI or WSB1 and CUL5.
INCEB1 and TCEB2), alongin A/TCB3 or SOCSI or WSB1 and CUL5.

INCEB1 CUL8, CUL5 and CUL7. Probably interacts with CDC34.
-!- SUBCELULAR LOCATION: Cycoplasmic and nuclear (By similarity).
-!- TISSUE SPECIFICITY: Widely expressed.
-!- DOMAIN: The RING-type zinc finger domain is essential for ubiquitin ligase activity. It coordinates an additional third zinc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IDENTIFICATION IN E3 UBIQUITIN LIGASE COMPLEX WITH MUF1, AND IDENTIFICATION IN COMPLEXES WITH CULE.

MEDLINE=21380117; PubMed=11384984; DOI=10.1074/jbc.M103093200;

KAMUTA T., BUXIAN D., YAN Q., Schmidt S.L., Lane W.S., Querido E., Branton P.E., Shilatifard A., Conaway R.C., Conaway J.W.; Querido E., MM.f1, a novel Blongin BC-interacting leucine-rich repeat protein that can assemble with Cul5 and Rbx1 to reconstitute a ubiquitin ligase."; J. Biol. Chem. 276:29748-29753(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY: Belongs to the RING-box family. SIMILARITY: Contains 1 RING-type zinc finger.
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and mouse cDNA sequences.";
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(See http://www.isb-sib.ch/announce/
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PubMed=12477932; DOI=10.1073/pnas.242603899;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
Richardson P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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                                                                                                                                           MGD; MGI:1891829; RbxI.
InterPro; IPR001841; Znf_ring.
Pfam; PF00097, zf-C3HC4, 21.
PROSITE; PS50089; ZF RING 2; 1.
Metal-binding; Nuclear protein; Ubl conjugation pathway; Zinc;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 ASATSEECTVAWGVCNHAFHFHCISRWLKTRQVCPLDNREWEFQKYGH 108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 108;
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                                                                                                                                                                                                                                                                                             Zinc 1 (By similarity).
Zinc 1 (By similarity).
Zinc 3 (By similarity).
Zinc 3 (By similarity).
Zinc 3 (By similarity).
Zinc 3 (By similarity).
Zinc 2 (By similarity).
Zinc 1 (By similarity).
Zinc 1 (By similarity).
Zinc 2 (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     064174;
25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Hypothetical protein.
Xenopus laevis (African clawed frog).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6.6e-61;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 616;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No.
  entities requires a license agreement ((or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                            RING-type.
                                                             EMBL; AF140599; AAD29716.1; -.
EMBL, AK003159; BABAZ512.1; -.
EMBL; BC027396; -; NOT ANNOTATED_CDS.
EMBL; BC056992; AAH56992.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
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Matches 108; Conservative
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                                                                                                                                                                                                                                                                              Xenopodinae; Xenopus.
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                                                                                                                                                                                                                                                    Zinc-finger.
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CONFLICT
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A Strausberg R.L., Feingold B.A., Grouse J.B., Derge J.G.,

Altschul S.P., Zeeberg B. Buetow K.H., Schaefer C.F., Bhard N.K.,

Altschul S.F., Zeeberg B. Buetow K.H., Schaefer C.F., Bhard N.K.,

Altschul S.F., Zeeberg B. Buetow K.H., Schaefer C.F., Bhard N.K.,

Applicant R.F., Jordan H., Moore T., Max S.I., Wang J., Haish F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A platchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Brownstein M.J. Usdin T.B., Tooshiyuki S., Carninci P., Prange C.,

Raha S.S., Mockan P.J., McKernan K.J., Malek J.A., Gunzatne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A Rilalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

A Nilalon D.K., Maray D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Rahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

T. "Generation and initial analysis of more than 15,000 full-length human
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Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A., Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Nyers R.M., Butterfield Y.S., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J., Marra M.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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Brachydanio rerio (Zebrafish) (Danio rerio).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 108;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Klein S., Gerhard D.S.;
Submitted (SEP-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BC082183; AAH82183.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hypothetical protein.
SEQUENCE 108 AA; 12274 MW; 30FCSADF66096C0E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25-CCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 616; DB 2;
Pred. No. 6.6e-61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Scc...
100.0%; Pred. No. b...
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and mouse cDNA sequences.
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Best Local Similarity
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NCBI_TaxID=7955;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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InterPro; IPR001841; Znf_ring.
Pfam; PF00097; zf-C3HC4; 1.
PROSITE; PSS0089; ZF_RING_2; 1.
Meral-binding; Nuclear protein; Ubl conjugation pathway; Zinc; Zinc-finger.
                                                                                                                                                                                                                                                                                                                       12318 MW;
                                                                                                                                                                                                                                                                                                                                                       98.18;
                                                                                                                                                                                                                                                                                                                                                                         98.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Anopheles gambiae str. PEST
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                                                                                                                                                                                                                                                                                                                                                                                          106; Conservative
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                                                                                           Similarity
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108 AA;
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SEQUENCE
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                                                                                                                                                                                                                                                                   9
                                                                                                                                                                                                                                                                                     4 MAAAMDVDTPSGANSGASKKRFEVKKWNAVALWAWDIVVDNCAICRNHIMDLCIECQANQ 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and a F-box protein (By Similarity).

--- SUBCELLULAR LOCATION: Cytoplasmic and nuclear (By similarity).
--- TISSUE SPECIFICITY: Expressed in heart and kidney.
--- INDUCTION: During hyperosmotic stress and thermal stress.
--- DOMAIN: The RING-type 2 inc finger domain is essential for ubiquitin ligase activity. It coordinates an additional third zinc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the
                                                                                                                                                                                                                                                                 1 MAAAMDVDTPSGTNSGAGKKRFEVKKWNAVALWAWDIVVDNCAICRNHIMDLCIECQANQ

Pan F., Zarate J., Bradley T.M.;
"A homolog of the E3 ubiquitin ligase Rbx1 is induced during hyperosmotic stress of salmon."
Am. J. Physiol. 282:R1643-R1653(2002).
-1- FUNCTION: Component of the SCF (SKP1-CUL1-F-box protein) E3 ubiquitin ligase complex, which mediates the ubiquitination and subsequent proteasomal degradation of target proteins. Through the RING-type zinc finger, seems to recruit the E2 ubiquitination nerzyme, like CDC34, to the complex and brings it into close proximity to the substrate (By similarity).
-1- PATHWAY: Ubiquitin conjugation; third step.
-1- SUBUNIT: Part of SCF complexes, which consist of SKP1, CUL1, RBX1

                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Salmo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WEDLINE=22005592; PubMed=12010746; DOI=10.1152/ajpregu.00571.2001;
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0
                                                                                                                                                                                                                                                                                                                                     61 ASATSEECTVAWGVCNHAFHFHCISRWLKTRQVCPLDNREWEFQKYGH 108
                                                                                                                                                                                                                                                                                                                                                         ASATSEECTVAWGVCNHAFHFHCISRWLKTRQVCPLDNREWEFOKYGH 111
                                                                                                                                                                                             Score 605; DB 2; Length 111;
Pred. No. 1.1e-59;
                                                                                                                                                                                                                               2; Indels
                                                                    Director MGC Project,
Submitted (SEP-2004) to the EMBL/GenBank/DDBJ databases
EMBL; BC081497; AAH81497.1; -.
                                                                                                                                                          111 AA; 12572 MW; 37E75920442DC9F6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A., TISSUE SPECIFICITY, AND INDUCTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
RING-box protein 1 (Rbx1) (Hyperosmotic protein 21).
   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIMILARITY: Belongs to the RBX1 family. SIMILARITY: Contains 1 RING-type zinc finger.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            108 AA
                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AY027936; AAK29182.1; ALT_INIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1111111111111111111111111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Name=RBX1; Synonyms=SHOP21; Salmo salar (Atlantic salmon).
                                                                                                                                                                                             98.2%;
98.1%;
                                                                                                                                                                                                                               Matches 106; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                               Best Local Similarity
                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=8030;
                                                      TISSUE=Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          RBX1 SALSA
Q8QG64;
                                                                                                                                                         SEQUENCE
                                                                                                                                                                                             Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MAAAMDVDTPSATNSGASKKRFEVKKWNAVALWAWDIVVDNCAICRNHIMDLCIECQANQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MAAAMDVDTPSGTNSGAGKKRFEVKKWNAVALWAWDIVVDNCAICRNHIMDLCIECQANQ
                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukāryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Diptera, Nematocera, Culicoidea, Anopheles.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mitted (WAR-2002) to the EMBL/GenBank/DDBJ databases.
SIMILARITY: Contains 1 RING-type zinc finger.
CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ŝ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 ASATSEECTVAWGVCNHAFHFHCISRWLKTRQVCPLDNREWEFQKYGH 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 ASATSEECTVAWGVCNHAFHFHCISRWLKTRQVCPLDNREWEFQKYGH 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    87.6%; Score 539.5; DB 2; Length 174;
86.2%; Pred. No. 3.8e-52;
iive 5; Mismatches 5; Indels 5
                                                                                                                                                                                                                                                                                                                                                                                  Length 108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           preliminary data.

EMBL; AAAB01008900; EAA09407.1; -.
GO; GO:000151; C:ubiquitin ligase complex; IEA.
GO; GO:0004842; F:ubiquitin ligase activity; IEA.
GO; GO:0008270; F:ainc ion binding; IEA.
GO; GO:0016567; P:protein ubiquitination; IEA.
Flan: PF00097; Zf-C3HC4; I.
FROSITE; PS50089; ZF RING 2; I.
Metal-binding; Zinc; Zinc-finger.
                                                                                                                                                                                                                                                                                                                                                                                                                                       2; Indels
                                                                                                                                                                                                                                                                                                                             44C3EA712CEDC7BB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     174 AA; 20040 MW; E981973BC526D3A1 CRC64;
                                                                        Zinc 3 (By similarity).
Zinc 3 (By similarity).
Zinc 2 (By similarity).
Zinc 1 (By similarity).
Zinc 1 (By similarity).
Zinc 3 (By similarity).
Zinc 1 (By similarity).
Zinc 1 (By similarity).
Zinc 2 (By similarity).
Zinc 2 (By similarity).
(By similarity) (By similarity)
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01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                  ; DB 1;
1.4e-59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             174 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORFNames=ENSANGG00000007948
                                                                                                                                                                                                                                                                                                                                                                                  Score 604; DE
Pred. No. 1.46
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Anopheles Genome Sequencing Consortium, Submitted (MAR-2002) to the EMBL/GenBanl
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RECENTINE=CRIONENCE FROM N.A.

RECENTINE=CROUNCE FROM N.A.

RECENTINE=CROUNCE FROM N.A.

RADININE=CROUNCE FROM N.B.

RADININE=CROUNCE FROM N.B.

RADININE=CROUNCE FROM N.B.

RADININE FROM N.A.

RADINON BEAU A.A.

RADININE BAND A.A.

RADININE RADININE M.B.

RADININE BAND A.A.

RADININE BAND A.A.

RADININE RADININE BAND A.A.

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RADININE RADININE RADININE RADININE BAND.

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RADININE 
66 MDIDEEEFEAPTSSSSRGERKRFEVKKWNAVALWAWDIVVDNCAICRNHIMDLCIECQAN 125
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Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.
Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A.,
Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
                                                                           60 QASATSEECTVAMGVCNHAFHFHCISRWLKTRQVCPLDNREWEFQXYGH 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                       126 QASATSEECTVAMGVCNHAPHFHCISRWLKTRQVCPLDNREWEFQKYGH
                                                                                                                                                                                                                                                                                                                                                                                     Q9WSE1, 077429;
10-CCT-2003 (Rel. 42, Created)
10-CCT-2003 (Rel. 42, Last sequence update)
25-JAN-2005 (Rel. 46, Last annotation update)
25-JAN-2005 (Rel. 46, Last annotation update)
Name-Rocla; ORFNames=CG16982;
                                                                                                                                                                                                                                                                                                                                                         108 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Science 287:2185-2195(2000).
                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENOME REANNOTATION.
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                                                                                                                                                                                                                                                                                                                                                         DROME
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RESULT 7

RESULT 7

REA DROME

DAC Q9WSE1

DT 10-OCT

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Trends Genet...;

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Trends Genet...;

In PUNCTION: Component of the SCF (SKPI-CULI-F-box protein) E3

ubiquitin ligase complex, which mediates the ubiquitination and
subsequent proteasomal degradation of target proteins. Through the
RING-type zinc finger, seems to recruit the E2 ubiquitination
enzyme to the complex and brings it into close proximity to the
substrate. Required for the specific SCF-dependent proteolysis of
CI, but not that of ARM, suggesting that it also participates in
the selection of substrates inside the SCF complex.

--- PATHWAY: Ubiquitin conjugation; third step.
--- SUBUNIT: Part of a SCF complex consisting of Skpa (SKPI), Lin19
---- Inin19 and Slmb. Interacts directly with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- SUBCELLUTAR LOCATION: Nuclear and cytoplasmic.
-!- TISSUE SPECIFICITY: Widely expressed. Expressed in embryonic,
larval and adult tissues.
-!- DEVELOPMENTAL STAGE: Expressed both maternally and zygotically.
-!- DOMAIN: The RING-type zinc finger domain is essential for ubiquitin ligase activity. It coordinates an additional third zinc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=Berkeley; TISSUE=Embryo;
MEDLINE=22426066; PubMed=12537569;
Stapleton M., Carlson J.W., Brokstein P., Yu C., Champe M.,
George R.A., Guarin H., Kronmiller B., Pacleb J.M., Park S., Wan K.H.,
Rubin G.M., Celniker S.E.;
"A brosophila full-length cDNA resource.";
Genome Biol. 3:RESEARCH0080.1-RESEARCH0080.8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ASN-59 AND CYS-68.
MEDLINE=22057626; PubMed=12062088; DOI=10.1016/S1534-5807(02)00164-8; MeDLINE=22057626; PubMed=12062088; DOI=10.10.5 Duronio R.J.; Noureddine M.A., Donaldson T.D., Thacker S.A., Duronio R.J.; "Drosophila Rocia encodes a RING-H2 protein with a unique function in processing the Hh signal transducer Ci by the SCF B3 ubiquitin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-22736111; Pubmed=12850443; DOI=10.1016/S0168-9525(03)00146-X; Ou C.-Y., Pi H., Chien C.-T.; Control of protein degradation by E3 ubiquitin ligases in Drosophila
                                                                                                                                                           Benos P.V., Gatt M.K., Ashburner M., Murphy L., Harris D.,
Barrell B.G., Ferraz C., Vidal S., Brun C., Demailles J., Cadieu E.,
Dreano S., Gloux S., Lelaure V., Mottier S., Galibert F., Borkova D.,
Minana B., Kafatos F.C., Louis C., Siden-Kiamos I., Bolshakov S.,
Papagiannakis G., Spanos L., Cox S., Madueno E., de Pablos B.,
Modolell J., Peter A., Schoettler P., Werner M., Mourkioti F.,
Callister D.M., Campbell L.A., Dardamitsou A., Henderson N.S.,
McMillan P.J., Salles C., Tait E.A., Valenti P., Saunders R.D.C.,
                                                                                                                     STRAIN=Oregon-R;
MEDLINE=20196011; PubMed=10731137; DOI=10.1126/science.287.5461.2220;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SPECIFICITY, DEVELOPMENTAL STAGE, AND MUTAGENESIS OF
                                                                                                                                                                                                                                                                                                                                                                                      "From sequence to chromosome: the tip of the X chromosome of D.
"Annotation of the Drosophila melanogaster euchromatic genome:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=21391618; PubMed=11500045; DOI=10.1006/bbrc.2001.5394;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bocca S.N., Muzzopappa M., Silberstein S., Wappner P.; "Occurrence of a putative SCF ubiquitin ligase complex in
                                            Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             atom (By similarity).
-!- SIMILARITY: Belongs to the RING-box family.
-!- SIMILARITY: Contains 1 RING-type zinc finger.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Biochem. Biophys. Res. Commun. 286:357-364 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REVIEW ON E3 UBIQUITIN LIGASE COMPLEXES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INTERACTIONS WITH LIN19 AND SLMB.
                                                                                                                                                                                                                                                                                                                                                                                                                                        Science 287:2220-2222(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Dev. Cell 2:757-770(2002).
                              review.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      eye development.";
                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Drosophila.";
                                                                                                                                                                                                                                                                                                                                                                                                                     melanogaster.
                                                                                                                                                                                                                                                                                                                                                                           Glover D.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FUNCTION,
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Sasaki T., Matsumoto T., Yamamoto K., Sakata K., Baba T., Katayose Y., Nu J., Niimura Y., Cheng Z., Nagamura Y., Antonio B.A., Kanamori H., Nu J., Niimura Y., Cheng Z., Nagamura Y., Antonio B.A., Kanamori H., Antonio M., Antonio B.A., Hayashi M., Okamoto M., Ando T., Antia K., Hamada M., Harada C., Hijishita S., Honda M., Ichikawa Y., Idonuma A., Iijima M., Ikeda M., Ikeno M., Itoh T., Itoh T., Itoh Y., Iwabuchi A., Kamiya K., A Raraswa W., Katagiri S., Kikuta A., Kobayashi N., Kono I., Nachita K., Machara T., Mizuno H., Mizubayashi T., Mukai Y., Nakamura M., Namiki N., Negishi M., Ohta I., Ono N., Saji S., Sakai K., Shibata M., Shimokawa T., Shomura A., Song J., Takazaki Y., Terasawa K., Teuji K., Wak, K., Yamagata H., Yamane H., Yaoshiki S., Yoshihara R., Yukawa K., A Zhong H., Iwama H., Endo T., Itoh H., Hahn J.H., Kim H.I., Bun M.Y., M. Wan, M., Jiang J., Gojobori T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MAAAMDVDTPSGTNSGAGK-KRFEVKKWNAVALWAWDIVVDNCAICRNHIMDLCIECQAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Oryza sativa (japonica cultivar-group).
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Ehrhartoideae, Oryzeae, Oryza.
                                                                                        SanMiguel P., Shiloff B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               66 QASATSEECTVAMGVCNHAFHFHCISRWLKTRQVCPLDNSEWEFQKYGH 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                60 QASATSEECTVAWGVCNHAFHFHCISRWLKTRQVCPLDNREWEFQKYGH 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "The genome sequence and structure of rice chromosome 1.", Nature 420:312-316(2002).
                                                                                                                                                                                                                                                                                                                                                                                                      GO; GO:0000151; C:ubiquitin ligase complex; IEA.
GO; GO:0004842; F:ubiquitin-protein ligase activity; IEA.
GO; GO:0008270; F:zinc ion binding; IEA.
GO; GO:0016567; P:protein ubiquitination; IEA.
InterPro; IPRO1041; Zif ring.
Ffam; PF00097; zf-C3HC4; 1.
SMART; SM00184; RING; 1.
                                                                                                                                                                                                                                 Sasaki T., Matsumoto T., Katayose Y.;
Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases
-!- SIMILARITY: Contains 1 RING-type zinc finger.
EMBL, AF480496; AAL87158.1; --
EMBL, AP005844; BAD08109.1; --
Gramene; Q8S3S0; --
                                                                                     Park Y.-J., Rostoks N., Ramakrishna W., SanMiguel P., Sl
Ma J., Jiang Z., Kleinhofs A., Bennetzen J.;
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS50089; ZF RING 2; 1.
Metal-binding; Zinc; Zinc-finger.
SEQUENCE 114 AA; 12754 WW; 568C63E0D733DD5C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         85.0%; Score 523.5; DB 2
84.4%; Pred. No. 1.5e-50;
ive 6; Mismatches 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Putative ring-box protein.
Name=P0005A05.23; Synonyms=P0482C06.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. PubMed=12447438;
                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                         SEQUENCE FROM N.A.
      NCBI_TaxID=39947;
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                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 59
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
      to erroneous
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last amotation update)
Putative ring box-1 protein (Putative RING box protein 1).
Name=49D11.12; Synonyms=0SJNBD0060016.27-1;
Oryza sativa (japonica cultivar-group).
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          R GO; GO: 0005634; C: notebus; IDA.
R GO; GO: 0005634; C: notebus; IDA.
R GO; GO: 0004840; F: ubiquitin ligase complex; IDA.
R GO; GO: 0004840; F: ubiquitin conjugating enzyme activity; NAS.
R GO; GO: 0008270; F: zinc ion binding; NAS.
R GO; GO: 0007224; P: smoothened receptor signaling pathway; NAS.
R InterPro; IPRO101841; Znf. zing.
R Pfam; PF00097; Zf-C34(4)-1.
R PROSITE; PS50089; Zf-RING_2; 1.
R PROSITE; PS50089; Zf-RING_2; 1.
N Developmental protein; Metal-binding; Nuclear protein; Ubl conjugation pathway; Zinc, Zinc-finger.
I ZN FING 53 98 RING-type.
I DOMAIN 12 15 Poly-Ser.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          86.7%; Score 534; DB 1; Length 108; 87.2%; Pred. No. 9.4e-52;
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CAUTION: Ref.3 sequence differs from that shown due
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EMBL, AL031581; CAA20888.1; ALT_SEQ.
EMBL, AY119265; AAM51125.1; -.
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FlyBase; FBgn0025638; Rocla.
                              gene model prediction.
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                                                                                                                                                                                                                    10-0CT-2003 (Rel. 42, Created)
10-0CT-2003 (Rel. 44, Last sequence update)
10-0CT-2003 (Rel. 44, Last annotation update)
05-JUL-2004 (Rel. 44, Last annotation update)
RING-box protein la (RBXLa-At) (At-Rbx1;1) (RBXI-2).
Name=RBXIA; OrderedLocusNames=At5g20570; ORFNames=F7C8.160;
Arabidopsis thaliana (Mouse-ear cress).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                    6 DVDTP-----SGTNSGAG-----KKRFEVKKWNAVALWAWDIVVDNCAICRNH
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                                                               DB 2; Length 123;
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84.5%; Pred. No. 1.6e-50;
tive 4; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: Contains 1 RING-type zinc finger.
EMBL, AY302066; AAP57304.1, -.
GO, GO:00000151; C.ubiquitin. ligase complex; IEA.
GO, GO:000842; F:ubiquitin.protein ligase activity; IEA.
GO, GO:0016567; P:protein ubiquitination; IEA.
InterPro: IPR001841; Znf_ring.
Fram; PP00097; zf-C3H44; 1.
SMART; SM00184; RING; 1.
                                                                                                                           Indels
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Metal-binding; Zinc; Zinc-finger.
SEQUENCE 110 AA; 12591 MW; 0172C6CAB3FA2772 CRC64;
13625 MW; 38260146F7B4DBA7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Last sequence update)
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6e-50;
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:ive 5; Mismatches
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                                                                                                                           93; Conservative
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les 93; Conservative
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                                                                                               Local Similarity
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Populus tomentosa.
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B. Ockreez L.;

B. Subbitcher (And. 2001) to the EWB1/GenBank/DDB3/S004807;

E. Stantiche FRON M.A.;

E. Simpling N., Salamoto S., Kimara T. Moouthi T. Kawahina K.,

B. Makzaki N., Manck O. Wather S. Minner M. March. A. Nakayana S.,

Roharda M., Yamada W., Yanda W., Sato S., de la Bastide M.,

B. Makzaki N., Manco K., Okumura S., Shinpos. Trabetoin C., Wada T.,

Makazaki N., Manco K., Okumura S., Shinpos. Trabetoin C., Wada T.,

Matang E., Spiedel L., Gaol J., O'Shamptnesy A., Peteron E.,

B. Marzaki M., March W., Okumura S., Shinpos. Trabetoin C., Wada T.,

Matang E., Spiedel L., Gaol J., O'Shamptnesy A., Peteron E.,

B. Marzaki M., March W., Okumura S., Shinpos. Trabets S.,

B. Marzaki M., March W., Okumura S., Shinpos. Trabets S.,

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B. Marzaki M., March W., Okumura S., Shinpos. Trabets S.,

B. Marzaki M., March W., Walland W., Walland M., D., Barrell M., D.,

B. Marzaki M., March M., March M., Walland M., Marzaki M.,

B. Marzaki M., March M., March M., Malama M., Marzaki M.,

B. Marzaki M., Manch M., Marzaki M., Marzaki M., Marzaki M.,

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    higher level in tissues containing actively dividing cells. DOMAIN: The RING-type zinc finger domain is essential for ubiquitin ligase activity. It coordinates an additional third zinc
"Role of the Arabidopsis RING-H2 protein RBX1 in RUB modification and SCF function.";
                                                                                                                                                                                                            MEDLINE=22568282; PubMed=12682009; DOI=10.1093/emboj/cdg190;
Dharmasiri S., Dharmasiri N., Hellmann H., Estelle M.;
"The RUB/Nedd8 conjugation pathway is required for early development
                                                                                                                                                                                                                                                            J. 22:1762-1770(2003).
FUNCTION: Component of the SCF (SKP1-CUL1-F-box protein) E3 ubiquitin ligase complex, which mediates the ubiquitination and subsequent proteasomal degradation of target proteins. The SCF
                                                                             INTERACTIONS WITH CULL, CUL4, ASK1. AND ASK2.
MEDLINE=22370998; PubMed=12381738; DOI=10.1074/jbc.M204254200;
Lechner E., Xie D., Grava S., Pigaglio E., Planchais S.,
Murray J.A.H., Parmentier Y., Mutterer J., Dubreucg B., Shen W.-H.
                                                                                                                                               its down-
                                                                     FUNCTION, TISSUE SPECIFICITY, IDENTIFICATION IN SCP COMPLEX, AND
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Pfam; PP00097; zf-C3HC4; 1.
PROSITE; PS50089; ZF_RING_2; 1.
Retal-binding; Nuclear protein; Ubl conjugation pathway; Zinc; Zinc-finger.
                                                                                                                                      Genschik P.;
"The AtRbx! protein is part of plant SCF complexes, and its of
regulation causes severe growth and developmental defects.";
J. Biol. Chem. 277:50069-50080 (2002).
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EMBL, AF26833; -; NOT ANNOTATED_CDS.
EMBL, AY066913, AAM64477.1; -.
EMBL, AY072430, AAL62422.1; -.
EMBL, AY114719; AAM48038.1; -.
EMBL, AXI18181; BAC42804.1; -.
                                            Plant Cell 14:2137-2144(2002)
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"The Genome Sequence shown hare is derived from an EMBL/Genbank,DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                    3 AAMDVDT---PSG-----TNSGAGKKRFEVKKWNAVALWAWDIVVDNCAICRNHIMD 51
                                                                                                                                                                                                                                 2 ATLDSDVTMIPAGEASSSVAASSSNKKAKRFEIKKWSAVALWAWDIVVDNCAICRNHIMD 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   85
                                                                                                                                                                                                                                                                                 52 LCIECQANQASATSEECTVAMGVCNHAFHFICISRWLKTRQVCPLDNREWBFQKYGH 108
                                                                                                                                                                                                                                                                                                                         62 LCIECQANQASATSEECTVAMGVCNHAFHFHCISRWLKTRQVCPLDNSEWEFQKYGH 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26 GKPRFEVKKWNAVALWAWDIVVDNCAICRNHIMDLCIECQANQSSATSEECTVAWGICNH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18 GKKRFEVKKWNAVALWAWDIVVDNCAICRNHIMDLCIECQANQASATSEECTVAWGVCNH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
                                                                                                                           DB 1; Length 118;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               preliminary data.

EMBL; AABKO1000163; EAA33839_1; -.
GO; GO:0000151; C:ubiquitin ligase complex; IEA.
GO; GO:00004870; F:ubiquitin-protein ligase activity; IEA.
GO; GO:0008270; F:zinc ion binding; IEA.
GO; GO:0016567; P:protein ubiquitination; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              82.0%; Score 505; DB 2; Length 11 94.4%; Pred. No. 1.7e-48; ive 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR001841; Znf_ring.
Pfam; PF00097; zf-C3H04; 1.
PROSITE; PS50089; ZF_RING_2; 1.
Hypothetical protein; Metal-binding; Zinc; Zinc-finger.
SEQUENCE 116 AA; 13168 MW; BF1D46357C40D802 CRC64;
92 Zinc 3 (By similarity).
93 Zinc 1 (By similarity).
104 Zinc 2 (By similarity).
1107 Zinc 2 (By similarity).
113238 MW; 19947BF06F442A82 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
                                                                                                                                          Pred. No. 1.5e-49;
6; Mismatches 8
                                                                                                                           Score 514.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Created)
                                                                                                                         83.5%;
78.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAR-2004 (TrEMBLrel. 26, 01-MAR-2004 (TrEMBLrel. 26, 01-MAR-2004 (TrEMBLrel. 26, 01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                            Local Similarity 78.6
nes 92; Conservative
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  92
93
104
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118 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Name=NCU06224.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=5141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=OR74A;
                                                                                                                         Query Match
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                                                                                   SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q7SBT1;
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Matches
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regulation causes severe growth and developmental defects.";
J. Biol. Chem. 277:50699-50080(2002).
-!- FUNCTION: Potential component of the SCF (SKP1-CUL1-F-box protein)
B3 ubiquitin ligase complex, which mediates the ubiquitination and
subsequent proteasomal degradation of target proteins. The SCF
complex plays a crucial role in regulating response to auxin and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-22204438; PubMed-12215511;
Gray W.M., Hellmann H., Dharmasiri S., Estelle M.;
"Role of the Arabidopsis RING-H2 protein RBX1 in RUB modification and
                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE SPECIFICITY.
MEDLINE-22370998; PubMed=12381738; DOI=10.1074/jbc.M204254200;
Lechner E., Xie D., Grava S., Pigaglio E., Planchais S.,
Murray J.A.H., Parmentier Y., Mutterer J., Dubreucg B., Shen W.-H.,
                                                                                                                                                                                                                                                         10-OCT-2003 (Rel. 42, Last sequence update)
05-UUL-2004 (Rel. 44, Last annotation update)
Putative RING-box protein 1b (RBX1b-At) (At-Rbx1,2) (RBX1-1).
Name=RBX1B; OrderedLocusNames=At3942830; ORFNames=T21C14.50;
Arabidopsis thaliana (Mouse-ear cress).
                        115 AA
78 AFHFHCISRWLKTRQVCPLDNREWEFQKYG 107
                                                                                                                                                                                                                                      Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Plant Cell 14:2137-2144 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nature 408:820-822(2000).
                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DISCUSSION OF SEQUENCE.
                                                                                                                                                                                                                                   0-OCT-2003 (Rel. 42,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           function."
                                                                                                                                                                                  RBXB ARATH
Q9M2B0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   67
is essential for growth and development. Through the RING-type zinc finger, seems to recruit the B2 ubiquitination enzyme, to the complex and brings it into close proximity to the substrate (By
                                                                                                                                                                ubiquitin ligase activity. It coordinates an additional third zinc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10 MGESSSISVPS--SSSKNSKRFELKKWSAVALWAWDIVVDNCAICRNHIMDLCIECLANQ
                                                              -!- PATHWAY: Ubiquitin conjugation; third step.
-!- SUBUNIT: Potential part of SCF complexes, which consist of a SKPl-related protein, a cullin, a RBX protein and a F-box protein.
-!- SUBCELLUIAR LOCATION: Nuclear and cytoplasmic (By similarity).
-!- TISSUE SPECIFICITY: Not detected in floral buds, stems and roots.
-!- DOMAIN: The RING-type zinc finger domain is essential for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MAAAMDVDTPSGTNSGAGKKRFEVKKWNAVALWAWDIVVDNCAICRNHIMDLCIECQANQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Mecazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ASATSEECTVAWGVCNHAFHFHCISRWLKTRQVCPLDVCEWEFQKYGH 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 ASATSEECTVAWGVCNHAFHFHCISRWLKTRQVCPLDNREWEFQKYGH 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 115;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12999 MW; 1515E3E417DB1FAF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; lervosco, control of the property of the process of the process of the protein; Metal-binding; Nuclear protein; Hypothetical protein; Metal-binding; Nuclear protein; Ubl conjugation pathway; Zinc; Zinc; Finger. 107 RING-type...milarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (By similarity).
                                                                                                                                                                                                -!- SIMILARITY: Belongs to the RBX1 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8.1e-48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        81.0%; Score 499; DB 1;
81.5%; Pred. No. 8.1e-48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q23457; Q8WSQ1;
10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Name=rbx-1; ORFNames=ZK287.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5, Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Zinc 1
Zinc 3
Zinc 3
Zinc 2
Zinc 2
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Zinc 2
Zinc 1
Zinc 1
Zinc 3
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                                                                                                                                                                                                                                                                                                                                                                                            PIR; T47341; T47341.
InterPro; IPR001841; Znf_ring.
                                                                                                                                                                                                                                                                                                                                                                             EMBL; AL138639; CAB87200.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        88; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             449
663
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          115 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
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METAL
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RBX1_CAEEL
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                                                                                                        SUBCELLULÂR LOCATION: Cytoplasmic and nuclear (By similarity). DOMAIN: The RING-type zinc finger domain is essential for ubiquitin ligase activity. It coordinates an additional third zinc
                                                                                                                                                                                                                                           PATHWAY: Ubiquitin conjugation, third step.
SUBUNIT: Part of SCF complexes, which consist of a SKP1 or a SKP1-related protein, a cullin protein, and a F-box protein (By
                                                                                                                                                                                                                                                                                                                                                           SIMILARITY: Belongs to the RING-box family.
SIMILARITY: Contains 1 RING-type zinc finger.
CAUTION: It is uncertain whether Met-1 or Met-10 is the initiator.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR001841; Znf_ring.
Pfam; PP00097; zf-C3HC4; 1.
SMART; SM00184; RING; 1.
PROSITE; PS50089; ZP RING 2; 1.
Metal-binding; Nuclear procein; Ubl conjugation pathway; Zinc;
                            The C. elegans sequencing consortium;
"Genome sequence of the nematode C. elegans: a platform for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 493; DB 1; Length 110;
Pred. No. 3.6e-47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             zinc 1 (By similarity).
zinc 1 (By similarity).
zinc 3 (By similarity).
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zinc 2 (By similarity).
zinc 2 (By similarity).
zinc 2 (By similarity).
zinc 1 (By similarity).
zinc 3 (By similarity).
zinc 6 (By similarity).
zinc 7 (By similarity).
zinc 2 (By similarity).
zinc 2 (By similarity).
zinc 2 (By similarity).
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EFE50F7684B30A56 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AB077287; BAB83695.1; ALT_INIT.
STRAIN=Bristol N2;
MEDLINE=99069613; PubMed=9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PIR; T27823; T27823.
WormBase; WBGene000004320; rbx-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12760 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  80.0%;
                                                        investigating biology.";
Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; Z70757; CAA94801.1; -.
                                                                                                  SEQUENCE OF 2-110 FROM N.A
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STRAIN=9724;

WEDLINE=21648401; PubMed=11859360; DOI=10.1038/nature724;

WEDLINE=21648401; PubMed=11859360; DOI=10.1038/nature724;

WOOD V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,

Squores J., Peat N., Hayles J., Basham D., Bowman S.,

Brocks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,

A conlins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,

Gollins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,

A collins M., Connor R., Cronin A., Davis P., Hidaley J., Modgson G.,

A Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,

A money P., Woule S., Mungall K., Murphy L., Miblett D., Odell C.,

A money P., Wolels S., Mungall K., Murphy L., Miblett D., Odell C.,

A Reteron J., Simmonds M., Squares R., Stevens K.,

A Reteron J., Simmonds M., Squares R., Stevens K.,

A skelton J., Simmonds M., Squares R., Squares S., Stevens K.,

A skelton J., Volckaert G., Aert R., Robben J., Grymonprez B.,

Weltjens I., Vanderreels E., Rieger M., Schaefer M., Mullett-Anuer S.,

A capier C., Fuchs M., Fritzc C., Holzer E., Mocstl D., Hilbert H.,

B ger P., Zimmermann W., Wedler M., Sancher M., Murselle B.,

Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,

Lucas M., Rochet M., Gaillardin C., Moore K., Hurst S.M.,

Lucas M., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,

Cerutti L., Lower T., McCombie W.R., Paulsen I., Potashkin J.,

A Conttei I., Lowe T., Moreno S., Armstrong J., Forsburg C.,

A Shakovski G.V., Ussery D., Barrell BG., Murse P.,

The genome sequence of Schizosaccharomyces pombe.";

Natical R., Rochet W. R., R., Pauler S., Murse P.,

The genome sequence of Schizosaccharomyces pombe.";
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SUBUNIT: Part of a SCF B3 ubiquitin ligase complex containing psh1, pipl, pcull and the F-box proteins popl and pop2. Instead of the popl/pop2 hetereodimer also homooligomers of popl or pop2 may be present in the complex.
SUBCELLULAR LOCATION: Nuclear and cytoplasmic.
DOMAIN: The RING-type zinc finger domain is essential for ubiquitin ligase activity. It coordinates an additional third zinc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FUNCTION: Component of B3 ubiquitin ligase SCF complexes, which mediate the ubiquitination and subsequent proteasomal degradation of target proteins. Seems to recruit the B2 ubiquitination enzyme. like UBC3/CDC34, to the complex and brings it into close proximity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A., FUNCTION, SUBCELLULAR LOCATION, AND INTERACTIONS WITH POPL? AND DCUL1.
MEDINE-2232532; PubMed-12167173; DOI=10.1186/1472-2091-3-22,
Seibert V., Prohl C., Schoultz I., Rhee E., Lopez R., Abderazzag K.,
Zhou C., Wolf E.A.,
Combinatorial diversity of fission yeast SCF ubiquitin ligases by homo-and heterooligomeric assemblies of the F-box proteins Poptp and
                                                                                                                                                                                                                              28-FEB-2003 (Rel. 41, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
RING-box protein pipl (Pop-interacting protein 1) (RING-box protein
60 ANQAAGLKDECTVAWGNCNHAFHPHCISRWLKTRQVCPLDNREWEFQKYGH 110
                                                                                                                                                                                                                                                                                                                                                       Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                       107 AA.
                                                                                                                                                                                                                                                                                                                                    Name=pip1; ORFNames=SPAC23H4.18C;
                                                                                                                                                       RBX1 SCHPO STANDARD; 1
013959;
28-FEB-2003 (Rel. 41, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BMC Biochem. 3:22-22(2002).
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NCBI_TaxID=4896;
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                                                                                                        RESULT 15
RBX1 SCHPO
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57 59

4; Gaps

14; Indels

5; Mismatches

88; Conservative

Matches

g 8

8

Local Similarity

1 MAAAMD---VDTPSGTNSGAGKKRFEVKKWNAVALWAWDIVVDNCAICRNHIMDLCIECQ 1 MAQASDSTAMEVEBATNQTV-KKRFEVKKWSAVALWAWDIQVDNCAICRNHIMDLCIECQ

58 ANQASATSEECTVAWGVCNHAFHFHCISRWLKTRQVCPLDNREWEFQKYGH 108

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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InterPro; IPR01841; Znf_ring.
Pfam; PF00097; zf-C3HC4; 1.
Pfam; PF00097; zf-C3HC4; 1.
PROSITE; PSS0089; ZF RING; 2; 1.
Metal-binding; Nuclear protein; Ubl conjugation pathway; Zinc; Zinc-finger.
Zinc-finger.
ZN FING 52 97 RING-type.
METAL 41 2inc 1 (By similarity).
METAL 44 44 Zinc 1 (By similarity).
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Pred. No. 1.7e-44;
4; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                     Zinc 1 (By similarity).
Zinc 1 (By similarity).
Zinc 3 (By similarity).
Zinc 3 (By similarity).
Zinc 3 (By similarity).
Zinc 3 (By similarity).
Zinc 2 (By similarity).
Zinc 2 (By similarity).
Zinc 1 (By similarity).
Zinc 1 (By similarity).
Zinc 1 (By similarity).
Zinc 2 (By similarity).
-!- SIMILARITY: Contains 1 RING-type zinc finger.
                                                                                                                                    EMBL, AF179228; AAD54393.1; -.
EMBL; Z98977; CAB58559.1; -.
PIR; T38310; T38310.
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Local Similarity 87.5%;
les 77; Conservative 4
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Best Local S
Matches 77
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Search completed: June 23, 2005, 15:29:44 Job time : 179 secs

FHCISRWLKTRQVCPLDNREWEFQKYGH 108

81

8 & 8

GenCore veraion 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd.	OM nucleic - nucleic search, using sw model	n: June 24, 2005, 00:17:37 ; Search time 2063 Seconds (without alignments) 7680.492 Million cell undates/sec
	OM nucleic -	Run on:

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Title: Perfect score:	US-09-541-462B-1 327
Sequence:	l atggcggcagcgatggatgttccaaaagtatgggcactag 327
Scoring table: IDENTITY_NUC	IDENTITY_NUC

Gapext 1.0	24227607955 residues
IDENTITY NUC	4708233 seqs, 24227607955
Scoring table:	Searched:

94		
Total number of hits satisfying chosen parameters:		
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Minimum Maximum Listing	GenEmbl:*
Post-processing: Minimum Match 0% Maximum Match 100 Listing first 45	Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	AF142059 Homo sapi CQ698451 Sequence CQ695007 Sequence CQ712328 Sequence CQ712142 Sequence CQ711142 Sequence AX888031 Sequence BD027641 Sequence BD027641 Sequence BD027641 Sequence BD017520 Wonlippel AF140598 Homo sapi CQ701366 Sequence BC017370 Homo sapi CQ832496 Sequence CQ709825 Sequence CQ709825 Sequence CQ709825 Sequence CQ709825 Sequence CQ709825 Sequence
SUMMARIES	AF142059 CQ698451 CQ695099 CQ695007 CQ712328 CQ711142 AX888031 BD27641 CQ72989 BD271520 AF140598 CQ701366 CQ701466 CQ701466 CQ701466 CQ701369 BC017370 CQ932496 CQ932496 CQ932496 CQ933737 HUMXQ60A05
DB	
% Query Match Length DB	327 433 463 463 471 472 482 503 503 503 535 535 635 636 6476 4476
% Query Match	100.00 10
Score	327- 327- 327- 327- 327- 327- 327- 320- 316- 308-8-30-8-30-8-30-8-30-8-30-8-30-8-30
Result No.	C - 1122 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1

AX281690 Sequence	Х73608 Н. варіепв ш	BD271522 VonHippel	AF140599 Mus muscu	BC082183 Xenopus 1	BC051473 Mus muscu	BC056992 Mus muscu	BC027396 Mus muscu	AY099360 Homo sapi	AYSSS280 Mus muscu	AC112970 Mus muscu	CQ702730 Sequence		CQ705678 Sequence	CR390140 Gallus ga	AR277693 Sequence	ARS42209 Sequence	AX212267 Sequence	CQ703590 Sequence	CQ713285 Sequence	BC081497 Danio rer	AY027936 Salmo sal	AC109638 Homo sapi	G27926 human STS S	AC123343 Rattus no	AC103413 Rattus no	
AX281690	HSTEST	BD271522	AF140599	BC082183	BC051473	BC056992	BC027396	AY099360	AY555280	AC112970	CQ702730	CQ707821	CQ705678	CR390140	AR277693	AR542209	AX212267	CQ703590	CQ713285	BC081497	AY027936	AC109638	G27926	AC123343	AC103413	
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92.1	8.06	88.7	88.7	88.7	88.7	88.7	88.7	88.2	87.8	87.3	85.9	35.2	83.7	77.7	9.77	77.6	77.6	76.1	73.1	72.6	72.1	70.8	70.3	68.6	9.89	
301.2		290.2	290.2				290.2	288.4	287	285.4	281		273.8	254	253.6		253.6	249	. 533	237.4	235.8	231.6	230	224.4	224.4	
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ALIGNMENTS

- 73 F:	Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 327) Obta,T., Michel,J.J., Schottelius,A.J. and Xiong,Y. ROCI, a homolog of APC11, represents a family of cullin partners with an associated ubiquitin ligase activity Mol. Cell 3 (4), 535-541 (1999)	10230407 2 (bases Ohta,T., Direct Su Submitted Universit Manning D	1327 1	1127 /gene="ROC1" /gene="ROC1" /good="Cullin partnering protein with associated ubiquitin ligase activity" /good="Cod1" sart=1 /product="RING finger protein" /protein_id="AaD30146.1" /bortein_id="AaD30146.1" /translation="WAAAMDYDFGSTNSGAGKKRPEVKKWNAVALWAWDIVVDNCAI CRNHIMDLCIECQANQASATSEECTVAWGVCNHAFHFHCISRWLKTRQVCPLDNREWE FQKYGH"
RESULT 1 AF142059 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM	REFERENCE AUTHORS TITLE JOURNAL MEDLINE	PUBMED REFERENCE AUTHORS TITLE JOURNAL	source	CDS

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              TTCCACTGCATCTCTCGCTGGCTCAAAACACGACAGGTGTGTCCATTGGACAACAGAGAG 300
                              260 TTCCACTGCATCTCTCGCTGGCTCAAAACACGACAGGTGTGTCCATTGGACAACAGAGAG 319
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Momo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                        Liew,C.C., Marshall,W.E. and Zhang,H.
Compositions and methods relating to osteoarthritis
Patent: WO 02070737-A 35025 12-SEP-2002;
Chondrogene Inc. (CA)
Location/Qualifiers
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                                                                                                                                                                                             453 bp DNA Sequence 35025 from Patent WO02070737. CQ690099.1 GI:42225827
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CQ695007
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
                                                                                                  320 TGGGAATTCCAAAAGTATGGGCACTAG 346
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                 Length 327;
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Compositions and methods relating to osteoarthritis
Patent: WO 02070737-A 43377 12-SEP-2002;
Chondrogene Inc. (CA)
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Best Local Similarity 100.0%; Pred. No. 1.4e-90;
Matches 327; Conservative 0; Mismatches 0;
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                                100.0%; Score 327; DB 9; 100.0%; Pred. No. 1.4e-90;
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CQ698451
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Compositions and methods relating to osteoarthritis
Patent: WO 02070737-A 56068 12-SEP-2002;
Chondrogene Inc. (CA)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 327; DB 6; Length 4 100.0%; Pred. No. 1.4e-90; ive 0; Mismatches 0; Indels
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Sequence 56068 from Patent W002070737.
CQ711142.1 GI:42271999

    472
    /organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

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Best Local Similarity 100.
Matches 327; Conservative
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo
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                       Liew,C.C., Marshall,W.E. and Zhang,H.
Compositions and methods relating to osteoarthritis
Patent: WO 02070737-A 39933 12-SEP-2002;
Chondrogene Inc. (CA)
Location/Qualifiers
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Compositions and methods relating to osteoarthritis
Patent: WO 02070737-A 57254 12-SEP-2002;
Chondrogene Inc. (CA)
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Seguence 57254 from Patent WO02070737.
CQ712328
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    .471
    /organism="Homo sapiens"
    /mol_type="unassigned DNA"
    /db_xref="taxon:9606"

                                                                                                                                                                      /organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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C12P21/02, C12P21/08, C12Q1/68//G06F17/30, C12N15/00, C12N5/00, PC
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                             Homo sapiens (human)
JP 2001269182-A/3887
02-OCT-2001
24-EEB-2000 JP 2000118773
34-FEB-1999 US 60/122487
JGRAN BAPUTIST DUMAS MILNE EDWARDS, BIMERIC DUCLAIR, JEAN YVES
                                                                                                                                                            C12N15/09, C07K14/435, C07K16/18, C12N1/15, C12N1/19, C12N1/21,
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Patent: JP 2001269182-A 3887 02-OCT-2001;
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/db_xref="taxon:9606"
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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/note="unnamed protein product"
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          AX888031
Sequence 3894 from Patent EP1033401.
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AF140598 508 bp mRNA linear PRI 11-MAY-1999
Homo sapiens ring-box protein 1 (RBX1) mRNA, complete cds.
AF140598
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Kamura, T., Koepp, D.M., Conrad, M.N., Skowyra, D., Moreland, R.J., Conaway, R.C., Harper, J.W. and Conaway, J.W.
Conaway, R.C., Harper, J.W. and Conaway, J.W.
Rbx1, a component of the VIL tumor suppressor complex and SCF ubiquitin ligaee.
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Kamura, T., Lane, W.S., Conaway, R.C. and Conaway, J.W.
Direct Submission
Submitted (15-APR-1999) Prog. Molec. Cell Biol., HHMI, Oklahoma
Med. Res. Fdn., 825 NE 13th St, Oklahoma City, OK 73104, USA
Location/Qualifiers
                                                                                                                                                          7 ATGGCGGCAGCGATGGATGCGCCGAGCGGCACCAACAACGAGGGGCGCAGCAAGAAG
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 508)
Conaway,J.W., Conaway,R.C. and Kamura,T.
VonHippel-Lindau tumor suppressor complex and novel component of
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Patent: JP 2002541775-A 1 10-DEC-2002;
OKLAHOWA MEDICAL RESEARCH FOUNDATION
OK Homo sapiens (human)
PN JP 2002541775-A/1
PD 10-DEC-2002
PP 25-FEB-1999 US 60/121787
PR 26-FEB-1999 US 60/121787
PI JOAN W CONAWAY, RONALD C CONAWAY, TAKUMI KAMURA PC
CIZNIS/09, A6IK38/00, A6IK38/53, A6IK45/00, A6IB35/00, CO7K14/47,
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Location/Qualifiers
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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    .508
    /organism="Homo sapiens"
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JP 2002541775-A/1.
Homo sapiens (human)
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Libsue Flocutement. Accordance of Health Intramural cDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing Dy: National Institutes of Health Intramural
Sequencing Center (NISC),
Gaithersburg, Maryland;
Web site: http://www.nisc.nih.gov/
Contact: nisc mgc@nhgri.nih.gov
Contact: nisc mgc@nhgri.nih.gov
Akhter.N., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B.,
Blakesley, R.W., Beckstrom-Sternberg, S.W., Benjamin, B.,
Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P.,
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Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Laric, P., Legaspi, R.,
Maduro, O.L., Maskeilo, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C.,
McDowell, J., Pearson, R., Stantripop, S., Thomas, P.J., Touchman, J.W.,
Tsurgeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L.,
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Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Klausner, R.D., Collins, F.S., Wagner, L., Schener, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N. K.,
Hopkins, R.F., Jordan, H., Moore, T., Waax, S.I., Wang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
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Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,
Morkerman, K.J., Malek, J.A., Gunzarne, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, B., Ketteman, M., Madan, A., Rodrigues, S.,
Sanchez, A., Whiting, M., Madan, A., Youug, A.C., Shevchenk, Y.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,
Butterfield, M. Schein, J. B., Jones, S.J. and Marra, M.A.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Strausberg R.
Direct Submission
Submitsion
Submitted (12-DEC-2000) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                      241 TICCACTGCATCTCGCTGGCTCAAAACACGACAGGTGTGTCCATTGGACAACAGAGAG
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On Sep 16, 2003 this sequence version replaced gi:12655214.
Contact: MGC help desk
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Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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Tissue Procurement: ATCC
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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100.0%; Score 327; DB 6; Length 523;
Best Local Similarity 100.0%; Pred. No. 1.4e-90;
Matches 327; Conservative 0; Mismatches 0; Indels
                                                                                                                   Length 508;
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Compositions and methods relating to osteoarthritis
Patent: WO 02070737-A 46292 12-SEP-2002;
Chondrogene Inc. (CA)
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Matches 327; Conservative 0; Mismatches 0;
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/protein_id="CAG30446.1"
| Dackein_id="G1:47678651"
| translation="madawDyDTPSGTNSGAGKKRFEVKKWNAVALWAWDIVVDNCAI
| CRNHIMDLCIECQANQASATSEECTVAWGVCNHAFHFHCISRWLKTRQVCPLDNREWE
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Homo sapiens ring-box 1, mRNA (cDNA clone IMAGE:4065797), partial
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larity 100.0%; Pred. No. 1.4e-90;
Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /mol_type="mRNA"
/db_xref="taxon:9606"
/chromosome="22"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              clone="pGEM.RBX1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /lab_host="JM109"
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19. .345
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     1. .535
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327; Conserv
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BC017370.1
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Best Local Si
Matches 327,
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BC017370
LOCUS
                                                                    REFERENCE
AUTHORS
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JOURNAL
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KEYWORDS
SOURCE
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                                                                 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAL Plate: 4 Row: j Column: 15. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /procein id="AAH01466.1"
/db_xref="G1:12655215"
/db_xref="IncousID:978"
/db_xr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GCGTCCGCTACTTCAGAAGAGTGTACTGTCGCATGGGGAGTCTGTAACCATGCTTTTCAC 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        186 GCGTCCGCTACTTCAGAAGAGTGTACTGTCGCATGGGGAGTCTGTAACCATGCTTTTCAC 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CGCTTTGAAGTGAAAAGTGGAATGCAGTAGCCCTCTGGGGCCTGGGATATTGTGGTTGAT 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="synonyms: ROC1, RNF75, BA554C12.1, MGC13357, MGC1481"
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                                                                                                                                                                                                     /organism="Homo sapiens"

//organism="mxNa"

//db xref="taxon:9606"

//clone="MGC:1481 IMAGE:3138751"

//tssue type="Placenta, choriocarcinoma"

//clone lib="NIH MGC_21"
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100.0%; Pred. No. 1.4e-90;
tive 0; Mismatches 0;
              Young, A., Zhang, L.-H. and Green, E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TGGGAATTCCAAAAGTATGGGCACTAG 327
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           db_xref="LocusID:9978"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'product="ring-box 1"
                                                                                                                                                                                                                                                                                                                                                                                                     'note="Vector: pOTB7"
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CR456560.1 GI:47678650
CDNA, chromosome 22; ORP.
Homo sapiens (human)
Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                     gene="RBX1"
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Matches 327; Conservative
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Gaps

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DEFINITION

RESULT 14 CR456560 ACCESSION VERSION KEYWORDS SOURCE ORGANISM

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Gaps ; 0 240

262

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142

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/db_xref="MIM:603814"
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VVDNCAICRNHIMDLCIECQANQASATSEECTVAMGVCNHAFHFHCISRWLKTRQVCP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 AACTGTGCCATCTGCAGGAACCACATTATGGATCTTTGCATAGAATGTCAAGCTAACCAG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 CGCTTTGAAGTGAAAAGTGGAATGCAGTAGCCCTCTGGGCCTGGGATATTGTGGTTGAT 120
                                                                                                                                       # 80. .346
//gene="RBXI"
//gene="RBXI"
//note="APCII, Component of SCF
ubiquitin ligase and anaphase-promoting complex
(Posttranalational modification, protein turnover,
chaperones / Cell division and chromosome partitioning]"
/db_xref="CDD:COG5194"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           203 GCGTCCGCTACTTCAGAAGAGTGTACTGTCGCATGGGGAGTCTGTAACCATGCTTTTCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23 ATGGCGGCAGCGATGGATGTGGATACCCCGAGCGGCACCAACAACAAGGGGCGCGGGGGAAGGAAG
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100.0%; Score 327; DB 9; Length 554;
Best Local Similarity 100.0%; Pred. No. 1.4e-90;
Matches 327; Conservative 0; Mismatches 0; Indels
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xref="LocusID:9978"
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Job time: 2069 secs
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                                                                                                 Strausberg, L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausberg, R.L., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Klausner, R.D., Collins, F.S., Wagner, L., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S. I., Wang, J., Haieh, F., Diatchenko, L., Marulana, K., Farmer, A.A., Rubin, G.M., Hong, L., Staplecon, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., McKernan, K.J., Malek, J.A., Gunarane, P.H., Richards, S.W., Wallalon, D.K., Mulahy, S.J., Bosak, S.A., McEwan, P. J., Hulyk, S.W., Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Ketteman, M., Gaven, E.D., Lokson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Wyers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E., Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAL Plate: 19 Row: c Column: 17 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 22091459. Location/Qualifiers
                       Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 554)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
Submitted (13-NOV-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     nstitute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Institute for Systems Biology
http://www.systemsbiology.org
contact: amadandsystemsbiology.org
Anup Madan, Jessica Fahey, Erin Helton, Mark Ketteman, Anuradha
Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="synonyms: ROC1, BA554C12.1, MGC13357, MGC1481,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        roc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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/tissue type="Brain, glioblastoma"
/tolone_lib="NIH MGC_57"
/lab_host="DHJOB"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NIH-MGC Project URL: http://mgc.nci.nih.gov
Conteat: MGC help desk
Email: ggapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         codon_start=2
/product="RBX1 protein"
/protein_id="AAH17370.2"
/db_xref="GI:32425477"
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/organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /mol_type="mRNA"
/db_xref="taxon:9606"
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Copyright (c) 1993 - 2005 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Aaa96882 Nuclectid Aac03896 Human sec Adg87496 Human tum Add87156 Human tum	Adg84881 Human tum Aaa74978 DNA encod Acn40951 Tumour-as	Ach29979 Human tes Ads09913 Human the	Add92179 Human aut Abv25615 Human aut Abv39512 Bovine ES	Aas94844 Human DNA Adf42703 Human Tes Adq18564 Human sof	Adg80865 Human SPA Adb7558 Prostate Adq23032 Human sof Aaa74980 DNA encod
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Claim 1; Fig 2A; 83pp; English

Aah97860 Murine 7-	Aah97862 Murine 7-	Aad12859 Human nov	Aah97861 Murine 7-	Aaa43288 Xenopus s	Aas86845 DNA encod		Abl22527 Drosophil				Adk56974 Plant DNA	Adr59906 Cotton cD	Adr59907 Cotton cD		Adk56881 Plant DNA	Adk56882 Plant DNA	Aad55694 Human THB	Adl08129 Human gen		Adk56888 Plant DNA	Adk56887 Plant DNA	Adp22559 Sea-squir	Adk56880 Plant DNA	Aat26036 Human gen
AAH97860	AAH97862	AAD12859	AAH97861	AAA43288	AAS86845	ACH27559	ABL22527	ADD17060	ADD17933	ADK55138	ADK56974	ADR59906	ADR59907	ACN55764	ADK56881	ADK56882	AAD55694	ADL08129	ADK56883	ADK56888	ADK56887	ADP22559	ADK56880	AAT26036
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282.8	282.8	253.6		219.2	_	205.8		191	191	191	191	190	188.4	186.8	184.6	184.4	183.8	183.8	182.8	182	182	180.8	175.6	174
21	22	23	24	25	26	27	28	c 29	c 30	c 31	c 32	33	34	c 35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

RESULT 1

ROC1; ROC2; cullin; ring finger protein; APC11; APC complex; SCF pathway; cullin dependent ubiquitin ligase; CDK inhibitor Sic1 degradation; Novel nucleic acid encoding cullin regulating ring finger proteins, termed as ROC proteins similar to anaphase-promoting complex 11, for therapeutic and diagnostic use. Nucleotide sequence of human ring finger protein ROC1. Location/Qualifiers
1. .327
/*tag= a
/product= "ROC1" BP. 31-MAR-2000; 2000WO-US008592. 99US-0127261P. 99US-0166927P. AAA96882 standard; DNA; 327 (UYNC-) UNIV NORTH CAROLINA. (first entry) WPI; 2000-647235/62. P-PSDB; AAB19160. Xiong Y, Ohta T; WO200058472-A2 Homo sapiens. 31-MAR-1999; 22-NOV-1999; 19-FEB-2001 05-OCT-2000. tumour; ss. AAA96882; Key **AAA**96882

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240
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The present sequence encodes a human ROC1 ring finger protein. The specification also describes human ROC2. ROC1 and ROC2 are similar to appecific about the APC complex. The proteins stimulate cullin dependent ubiquitin ligase activity. ROC1 functions in vivo as an essential regulator of CDK inhibitor Sic1 degradation by the SCF (undefined) pathway. ROC proteins are useful for screening bloactive agents that interfere with the binding of ROC proteins with cullin proteins. Pharmaceutical formulations comprising ROC proteins are useful for diagnostic and therapeutic purposes, preferably for diagnosing and
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0; Mismatches 0;
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The present sequence is one of a large number of 5' ESTB derived from mRNAs encoding secreted proteins. An ORF has been identified within the sequence. The 5' ESTB were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA libraries. Such ESTB are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer cDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTB are derived from mRNAs with inteact 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTB are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design expression and secretion
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obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and
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                                                                                                     Claim 1; SEQ ID NO 3894; 71pp + Sequence Listing; English
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186 GCGTCCGCTACTTCAGAAGAGTGTACTGTCGCATGGGGAGTCTGTAACCATGCTTTTCAC 245

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The present invention describes an isolated tumour-associated antigenic target (TAT) nucleic acid comprising: (a) any of 4522 nucleotide sequences see SEQ ID NO:1 to 4622); (b) the full-length coding region of (a); (c) the complement of (a) and (b); (d) a sequence that has 80% equences see SEQ ID NO:1 to 4622); (e) the full-length coding region of the complement of (a) an expression vector comprising the above comprising the above expression vector; (a) a process for producing a polypeptide; (4) an isolated polypeptide (a) an amino acid sequence encoded by any of the above nucleotide sequences for producing a polypeptide; (b) an isolated py any of the above nucleotide sequences; (b) an amino acid sequence encoded by the full-comprising the above polypeptide; (b) a comprising the above polypeptide; (b) a comprising the above polypeptide; (b) an isolated oligopeptide; (f) a process for producing the antibody; (a) an isolated oligopeptide; (f) a process for producing the antibody; (a) an isolated oligopeptide; (b) an isolated oligopeptide; (f) a process for producing the antibody; (a) an isolated oligopeptide; (f) a process for producing the antibody; (a) an isolated oligopeptide; (l) a nomposition of matter comprising the above protein; (in) a composition of matter comprising the above protein; (l) a mathod of a call that expresses the above protein; (l) a mathod of a call that expresses the above protein; (l) an article of manufacture comprising a container; (l) method of a call that expresses the above protein; (l) a method of a call that expresses the above protein; (l) a method of a call that expresses the above protein; (l) a method of a call that expresses the above protein; (l) a method of a call that expresses the above protein; (l) a method of a call that expresses the above protein; and (l) a method of binding an antibody, oligopeptide or colin; and (l) a method of binding an antibody, oligopeptide or a call that expresses the above protein; and (l) a method of diagnosing the presence of a procession an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cell proliferative disorder or cancer. The present sequence represents a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     preventing or treating cancer. The composition is also used for preparin
a medicament for the therapeutic treatment or diagnostic detection of a
                                                                                                                                                                                                                              New nucleic acid molecule and encoded polypeptide, for diagnosing, preventing or treating cell proliferative disorders such as cancer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     human TAT cDNA sequence from the present invention.
                                                                                                                                                                                                                                                                                                         Claim 1; SEQ ID NO 4374; 5504pp; English.
                     GENENTECH INC
                                                                                                                                                                           WPI; 2004-534300/51.
                                                (WUTD/) WU T D. (ZHOU/) ZHOU Y.
                                                                                                                           Wu TD, Zhou Y;
                        (GETH )
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120 66 CGCTTTGAAGTGAAAAGTGGAATGCAGTAGCCCTCTGGGCCTGGGATATTGTGGTTGAT 125 AACTGTGCCATCTGCAGGAACCACATTATGGATCTTTGCATAGAATGTCAAGCTAACCAG 185 GCGTCCGCTACTTCAGAAGAGTGTACTGTCGCATGGGGGAGTCTGTAACCATGCTTTTCAC 240 121 AACTGTGCCATCTGCAGGAACCACATTATGGATCTTTGCATAGAATGTCAAGCTAACCAG 180 9 65 CGCTTTGAAGTGAAAAGTGGAATGCAGTAGCCCTCTGGGCCTGGGATATTGTGAT Gaps ; 0 100.0%; Score 327; DB 12; Length 506; 100.0%; Pred. No. 4.4e-101; ative 0; Mismatches 0; Indels 0; Best Local Similarity 100. Matches 327; Conservative 126 9 181 Query Match g g 요 ઠે ઠે ઠ

cells that express the above protein; (14) a method of determining the

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The present invention describes an isolated tumour-associated antigenic target (TAT) nucleic acid comprising: (a) any of 4622 nucleotide sequences (see SEQ ID NO:1 to 4622); (b) the full-inapth coding region of (a); (c) the complement of (a) or (b); (d) a sequence that has 80% or (a); (c) the complement of (a) or (b); (d) a sequence that has 80% or (a) or (b); (d) a sequence that hybridises to (a).

CC sequence identity to (a)-(c); or (e) a sequence that hybridises to (a) a process for producing a polypeptide; (4) an isolated polypeptide (a) a process for producing a polypeptide; (4) an isolated polypeptide (c) a process for producing a polypeptide; (4) an isolated polypeptide (c) and amino acid sequence encoded by the full-comprising the above polypeptide (a) or (b); (5) a chimeric polypeptide (c) an isolated antibody that binds to the above polypeptide; (6) an isolated antibody that binds to the above polypeptide; (6) an isolated antibody that binds to the above polypeptide; (1) a composition of matter comprising the above polypeptide; (1) a composition of matter comprising the above polypeptide; (10) a composition of matter comprising the above polypeptide; (10) a composition of matter comprising the above polypeptide; (10) a composition of matter comprising the above polypeptide; (10) a composition of matter contained within the container; (11) an article of manufacture comprising a container and the containing effect of the above protein; (13) a method of containing the containing a method of containing the prowth of the cell is at least in part (dependent upon a growth containing a method of containing the above protein; (13) a method of deferentiating a manufacture comprising a method of the cell is at least in part (dependent upon a growth containing a method of the cell is at least in part dependent and comprising a containing a c
TICCACTGCATCTCTCGCTGGCTCAAAACACGACAGGTGTGTCCATTGGACAACAGAGAG 300
                            human; tumour-associated antigenic target; TAT; cytostatic; gene therapy;
cancer; cell proliferative disorder; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                          Human tumour-associated antigenic target (TAT) cDNA sequence #4032.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New nucleic acid molecule and encoded polypeptide, for diagnosing, preventing or treating cell proliferative disorders such as cancer.
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                                                                                                                                                                                                                                                                          ADQ87156 standard; cDNA; 506 BP.
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                                                                                                                                                                                                                                                                                                                                                                            (first entry)
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presence of a protein in a sample suspected of containing the protein described above; (15) methods of diagnosing the presence of a tumour in a mammal; (16) a method for treating or preventing a cell proliferative disorder associated with increased expression or activity of the above protein; and (17) a method of binding an antibody, oligopeptide or organic molecule to a cell that expresses the protein described above. The TAT sequences have cytostatic activities, and can be used in gene therapy. The composition and methods are useful for diagnosing, preventing or treating cancer. The composition is also used for preparing a medicament for the therapeutic treatment or diagnostic detection of a cell proliferative disorder or cancer. The present sequence represents a
                                                                                                                                                                                                                                                                                                                                                               human TAT cDNA sequence from the present invention.
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Sequence 506 BP; 126 A; 105 C; 124 G; 151 T; 0 U; 0 Other;

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TTCCACTGCATCTCTCGCTGGCTCAAAACACGACAGGTGTGTCCATTGGACAACAGAGAG 300
                                                                                                                                  61 CGCTTTGAAGTGAAAAAGTGGAATGCAGTAGCCCTCTGGGCCTGGGATATTGTGTGGTTGTT 120
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 Length 506;
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                 4.4e-101;
DB 12;
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100.0%; Score 327; 100.0%; Pred. No. 4
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ADQ84881 standard; cDNA; 506 BP (first entry) 07-OCT-2004 ADQ84881; RESULT 5 ADQ84881

human; tumour-associated antigenic target; TAT; cytostatic; gene therapy; cancer; cell proliferative disorder; gene; ss. Human tumour-associated antigenic target (TAT) cDNA sequence #1695.

WO2004060270-A2. Homo sapiens

22-JUL-2004.

15-OCT-2003; 2003WO-US029126. 18-OCT-2002; 2002US-0418988P

GENENTECH INC WU T D. ZHOU Y. (GETH) (WUTD/) W (ZHOU/) Z

Zhou Y; λι TD,

WPI; 2004-534300/51

preventing or treating cell proliferative disorders such as cancer nucleic acid molecule and encoded polypeptide, for diagnosing

Claim 1; SEQ ID NO 1695; 5504pp; English.

The present invention describes an isolated tumour-associated antigenic target (TAT) mucleic acid comprising; (a) any of 4622 nucleotide sequences (see SEQ INO: 1 to 4622); (b) the full-length coding region of carget (TAT) mucleic acid comprising; (a) any of 4622 nucleotide sequence identity to (a) -(c); or (e) a sequence that hybridises to (a) -(c). Also described: (l) an expression vector comprising the above expression vector; (3) a process for producing a polypeptide; (4) an isolated polypeptide occupation; (a) an amino acid sequence encoded by any of the above comprising the above expression vector; (3) a comprising the above polypeptide (b) an amino acid sequence encoded by the full-comprising the above polypeptide (sequence encoded by any of the above comprising the above polypeptide fused to a heterologous polypeptide; (6) an isolated antibody that binds to the above polypeptide; (6) an isolated antibody that binds to the above polypeptide; (6) an isolated antibody that binds to the above polypeptide; (10) a tumour associated antipody (17) a process the above polypeptide; (9) a tumour associated antipodic target (17x) chinding organic molecule that binds to the above polypeptide; (10) a tumour associated antipody of antipody of a cell that expresses the above polypeptide or TAT binding organic molecule, and binds to the above polypeptide; (11) an article of manufacture comprising a container and composition of matter contained within the container; (12) mathods of matter contained within the container; (12) mathods of containing the protein; (13) a method of determining the presence of a tumour in a described above; (15) methods of diagnosing the presence of a tumour in a described above; (15) methods of diagnosing the presence of a tumour in a method for treating or preventing a cell protler associated with increased expresses the above protein; (14) and expresses the above protein; (15) a method of diagnosing the presence of a protein in a sample enspected of containing the above; (15) methods of diag preventing or treating cancer. The composition is also used for preparing a medicament for the therapeutic treatment or diagnostic detection of a cancer. The present sequence represents a numan TAT cDNA sequence from the present invention. proliferative disorder or

Sequence 506 BP; 126 A; 105 C; 124 G; 151 T; 0 U; 0 Other;

ö Gaps .; 0 Length 506; Indels 100.0%; Score 327; DB 13; 100.0%; Pred. No. 4.4e-101; iive 0; Mismatches 0; Best Local Similarity 100. Matches 327; Conservative

65 6 ATGGCGGCAGCGATGGATGTGGATACCCCGAGCGGCACCAACAGCGGCGCGGGCAAGAAG

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120 125 180 61 CGCTTTGAAGTGAAAAGTGGAATGCAGTAGCCCTCTGGGCCTGGGATATTGTGGTTGAT 66 CGCTTTGAAGTGAAAAGTGGAATGCAGTAGCCCTCTGGGCCTGGGATATTGTGGTTGAT 121 AACTGTGCCATCTGCAGGAACCACTTATGGATCTTTGCATAGAATGTCAAGCTAACCAG 셤

185 240 126 AACTGTGCCATCTGCAGGAACCACATTATGGATCTTTGCATAGAATGTCAAGCTAACCAG 181 GCGTCCGCTACTTCAGAAGAGTGTACTGTCGCATGGGGAGTCTGTAACCATGCTTTTCAC 셤 ð ò

245 305 TTCCACTGCATCTCTCGCTGGCTCAAAACACGGCGGTGTGTCCATTGGACAACAGAGAG 300 146 TTCCACTGCATCTCTCGCTGGCTCAAAACACGACAGGTGTGTCCCATTGGACACACAGAGAG 186 GCGTCCGCTACTTCAGAAGAGTGTACTGTCGCATGGGGAGTCTGTAACCATGCTTTTCAC 241 ద ò

301 TGGGAATTCCAAAGTATGGGCACTAG 327

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The present sequence encodes a human cullin-interacting RING-H2 finger protein (Ring box protein), designated Rbx1. The polypeptide is a tumour suppressor. Rbx1 is useful for diagnosting a predisposition of a patient to certain carcinomas. It is also useful for treating Ring box protein associated carcinomas. It is also useful for treating Ring box protein animals. Rbx1 is also useful for evaluating the effectiveness of a therapeutic treatment for Ring box associated carcinomas. Rbx1 can be used to screen for agents which augment or inhibit the activity of other coullin-containing ubiquitin ligase and of the VHL (von Hippel- Lindau) complex controlling the conjugation of ubiquitin or ubiquitin-like proteins to various sets of target proteins. Carcinomas which may be treated include renal carcinomas, cereballar hemangioblastomas and hemangiomas, retinal angiomata and pheochromocytomas encoding a human cullin-interacting RING-H2 finger protein (Rbx1). Cullin interacting RING-H2 finger protein, a component of von Hippel-Lindau tumor suppressor complex and Skpl-Cdc53p-F-box protein (SCF) ubiquitin ligase, useful for diagnosing and treating Ring box protein "cullin-interacting RING-H2 finger protein Cullin-interacting RING-H2 finger protein; Ring box protein; Rbxl; tumour suppressor; carcinoma; Ring box associated carcinoma; von Hippel-Lindau complex; ubiquitin conjugation; renal carcinoma; cerebellar hemangiobastoma; hemangioma; retinal angiobata; 100.0%; Score 327; DB 3; Length 508; 100.0%; Pred. No. 4.4e-101; Sequence 508 BP; 126 A; 106 C; 124 G; 152 T; 0 U; 0 Other; Location/Qualifiers Kamura T; (OKLA-) OKLAHOMA MEDICAL RES FOUND Claim 3; Page 35; 37pp; English. ВР 99US-0121787P. 25-FEB-2000; 2000WO-US004838 __ag= a /product= "c (Rbx1)" AAA74978 standard; DNA; 508 (first entry) Conaway JA, Conaway RC, 7. .333 /*tag= pheochromocytomas; ss. associated carcinomas. WPI; 2000-572067/53. P-PSDB; AAB08813 WO200050445-A1 02-JAN-2001 26-FEB-1999; Homo sapiens 31-AUG-2000. 306 AAA74978; DNA **AAA7497**6 RESULT 셤

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300
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                                                                                                                                                                                                               The invention relates to human tumour-associated antigenic target (TAT) polypeptides, and their related nucleic acids. The TAT polypeptides are overexpressed in cancer tissues compared to normal tissues, and may thus serve as effective targets for the diagnosis and treatment of cancer in mammals. The invention also relates to nucleic acid and polypeptide sequences at least 80% identical to the TAT nucleic acids and polypeptide acids and polypeptides, expression vectors and host cells comprising a TAT nucleic acid; an antibody specific for a TAT polypeptide; a peptide or organic molecule which binds to a TAT polypeptide; fusion proteins comprising a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fumour-associated antigenic target (TAT) cDNA DNA326980, SEQ ID NO:6072.
                                               AACTGTGCCATCTGCAGGAACCACATTATGGATCTTTGCATAGAATGTCAAGCTAACCAG
                                                                     TTCCACTGCATCTCGCTCGCTCAAAACACGACAGGTGTGTCCATTGGACAACAGAGAG
CGCTTTGAAGTGAAAAAGTGGAATGCAGTAGCCCTCTGGGCCTGGGATATTGTGGTTGAT
                                                                                                                    GCGTCCGCTACTTCAGAAGAGTGTACTGTCGCATGGGGAAGTCTGTAACCATGCTTTTCAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New tumor-associated antigenic target polypeptides and nucleic acids, useful in preparing a medicament for treating or detecting a proliferative disorder, e.g. breast, lung, colorectal, ovarian or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tumour-associated antigenic target; TAT; human; overexpression; ct
tumour; diagnosis; cell proliferative disorder; breast cancer;
colorectal cancer; lung cancer; ovarian cancer; liver cancer;
central nervous system cancer; bladder cancer; pancreatic cancer;
cervical cancer; melanoma; leukaemia; hybridisation probe;
chromosome identification; chromosome mapping; gene mapping;
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TAT polypeptide; and methods and compositions for the treatment or diagnosis of cancer in mammals. TAT polypeptides, nucleic acids, antibodies, antagonists, binding molecules and compositions are useful for diagnosing or treating a cell proliferative disorder associated with increased TAT expression, particularly cancers such as breast cancer, colorectal cancer, lung cancer, varian cancer, liver cancer, bladder cancer, pancreatic cancer, ovarian cancer, liver cancer, bladder nervous system, melanoma and leukaemia. TAT nucleic acids may further be chromosome identification and in gene therapy. The present sequence represents a TAT nucleic acid of the invention
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Human; 88; sequencing by hybridisation; SBH; expressed sequence tag; EST; genome mapping; biodiversity; genetic disorder.
            ACH29979 standard; cDNA; 476
                                        (first entry)
                                                     Human testis cDNA #365.
                                                                                                    US2003073623-A1
                                                                                       Homo sapiens
                                        13-OCT-2003
                                                                                                                  17-APR-2003.
                          ACH29979
RESULT 8
ACH29979
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Human therapeutic DNA - SEQ ID 150. ADS09913 standard; DNA; 3726 BP (first entry) 16-DEC-2004 ADS09913 RESULT 9 ADS09913/c

> 30-JUL-2001; 2001US-00918995 30-JUL-2001; 2001US-00918995

LABAT I. STACHE-CRAIN B.

DICKSON M C. JONES L W.

DRMANAC R T.

(DRMA/) (LABA/) (STAC/) (JONE/) Jones LW;

Drmanac RT, Labat I, Stache-Crain B, Dickson MC,

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The invention relates to an isolated polymucleotide comprising any one of 38043 cDNA sequences, appearing as ACH12789-ACH50831, whose sequence was determined by the technique of SBH (sequencing by hybridisation). Also included is a purified polypeptide comprising a sequence corresponding to a reading frame of the novel polymoleotide. The nucleic acid sequences are useful in diagnostics as expressed sequence tags (EST) for informance; in forensics, in assessing biodiversities, or in identifying mutations in forensics, in assessing biodiversities, or in identifying mutations responsible for genetic disorders and other traits. The nucleotide for corresponding in the recombinant production of protein, or in generating antibodies specific for it. The present sequence is useful for generating antibodies specific for it. The present sequence is one of the 38043 isolated cDNA/EST sequences. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from 18770 at
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                                                New polynucleotide sequences obtained from various cDNA libraries, useful as hybridization probes, as oligomers for PCR, for chromosome and gene mapping, in the recombinant production of protein, or in generating antisense DNA or RNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         antiinflammatory; neuroprotective; antianaemic; cytostatic; vulnerary; inflammatory; haematopolesis; immunity; neurodegenerative; stem cell; aplastic anaemia; cancer; wound healing; gene therapy; ds; gene.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 476;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 476 BP; 119 A; 111 C; 124 G; 118 T; 0 U; 4 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 99.4%; Score 325; DB 9; Le Best Local Similarity 100.0%; Pred. No. 2.1e-100; Matches 325; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              seqdata.uspto.gov/sequence.html?DocID=20030073623
                                                                                                                                                          Claim 1; SEQ ID NO 17191; 44pp; English
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Breast cancer related marker, seg id 11311
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                                                                                                                                                                                                                                                                                             The invention relates to a novel isolated polynucleotide and the encoded polypeptide. The molecules of the invention demonstrate antinflammatory, neuroprotective, antianaemic, cyrostatic and vulnerary activities and may be useful in preparing a composition for diagnosing or treating inflammatory, haematopoiettc, immune, neurodegenerative or stem cell disorders, such as aplastic anaemia or cancer, as well as for promoting wound healing. The molecules may also be utilised during gene therapy procedures. The current sequence is that of a human therapeutic DNA of the invention. The current sequence is not shown explicitly within the specification but can be accessed from the WIPO web-site.
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                                                                                                                                                                                                                       New polynucleotide, useful in preparing a composition for diagnosing treating inflammatory, neurodegenerative or stem cell disorders, e.g. aplastic anemia or cancer for promoting wound healing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Gaps
                                                                                                                                               Tang YI, Asundi V, Ren F, Zhang J, Wehrman T, Wang Z, Ma Y; Wang D, Chen R, Zhao QA, Wang J, Ghosh M, Xue AJ, Weng G, '
                                                                                                                                                                                                                                                                                                                                                                                                                                                           98.4%; Score 321.8; DB 13; Length 3726; 99.4%; Pred. No. 7e-99; 2; Indels 0; ative 0; Mismatches 2; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 3726 BP; 996 A; 955 C; 845 G; 930 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                        Claim 1; SEQ ID NO 150; 718pp; English.
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1D ACN90161 standard; DNA; 4543
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AC ACN90161;
XX
XX
DT 02-DEC-2004 (first entry)
                                                                         30-SEP-2003; 2003WO-US030720
                                                                                                02-OCT-2002; 2002US-0416186P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 99.4
Matches 323; Conservative
                                                                                                                                                                                     WPI; 2004-668857/65
                                                                                                                          (NUVE-) NUVELO INC
                                                                                                                                                                                                  P-PSDB; ADS10597.
                        WO2004080148-A2
 Homo sapiens
                                                23-SEP-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel isolated polypeptide associated with breast cancer, useful for detecting presence of polypeptide in sample, as a marker for breast
Cancer; breast; tumour; cytostatic; marker; detection; therapy; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 11; Length 4543;
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18.4%; Score 321.8; DB 11; Length
al Similarity 99.4%; Pred. No. 7.7e-99;
323; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure, SEQ ID NO 11311; 36pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lillie J, Xu Y, Wang Y, Steinmann K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          303 GGAATTCCAAAAGTATGGGCACTAG 327
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                                                                                                                                                                                                                                                                                                       18-JUL-2002; 2002US-00198846.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             (MILL-) MILLENNIUM PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2003-787014/74.
                                                                                                                                                 US2003099974-A1
                                                                              Homo sapiens.
                                                                                                                                                                                                                            29-MAY-2003.
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RESULT 11 ADQ92179

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This invention describes now accors; prokaryotic or entaryotic cells; produce recombinant expression vectors; prokaryotic or entaryotic cells; poly- or mono-clonal antibodies (Ab) specific; hybridomas that express monoclonal Ab; biosensor chips having an addressable sequence pattern as monoclonal Ab; biosensor chips having an addressable sequence pattern as probes; medical or diagnostic instruments that include the biosensor; for extracorporcal differential diagnosis of autoimmune diseases and proteins tubulins; dolichyl-diphospho-oligosacharide-glycosyl transferases and proteins. The autoantisosacharide-glycosyl transferases and proteins. The autointospho-oligosacharide-glycosyl transferases and proteins. The antibodies may be labelled conventionally with radioisotopes, coloured or fluorescent groups, or a member of the option, avidin pair, or colloidal gold. The autoantigens can be directed against mitochondria, liver-kidney microsomes; histidyl-tRNA; nuclear membrane, neutrophilin/cytoplasm; insect cells; epidermal intracellular cor basal membrane antigens; gold or cell nuclei, or associated with multiple sclerosis or rheumatoid arthritis. They are useful for epitope mapping; in affinity chromatography or electrophoresis; for diagnosis, produce biosensor chips or for autoantibody apheresis.

C autoantigen DNA can be used for therapeutic response of autoimmune diseases; to produce biosensor chips or far autoantibody apheresis.

C autoantigen DNA can be used for therapeutic RNA interference against autoantibodies. Blochips that carry the new materials are useful in medical and diagnostic instruments. AD092020-AD092280 represent human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New human DNA autoantigens, useful as assay, diagnostic, and prognostic reagents and for treating autoimmune disease, also related expression products and antibodies with similar uses.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              invention describes novel human DNA autoantigens which are used to
                                                                                                                                                                                                                                                                                                                                                ribosomal protein; tubulin; dollaring disparate disposal protein; tubulin; dollaring dollaring tubulin; dollaring dollaring dollaring disparate di
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 503 BP; 131 A; 102 C; 120 G; 150 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                              ds; autoantigen; antibody; hybridoma; biosensor chip; extracorporeal differential diagnosis; autoimmune disease;
                                                                                                                                                                                                                     Human autoantigen DNA fragment MPMGp800L05536.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   97.9%; Scor.
100.0%; Pred. No. 1.-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; SEQ ID NO 160; 110pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23-DEC-2002; 2002WO-EP014731
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23-DEC-2002; 2002WO-EP014731
   ADQ92179 standard; DNA; 503
                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              rhiesen H, Lorenz P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2004-543459/52.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (THIE/) THIESEN H. (LORE/) LORENZ P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO2004058972-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
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                                                                            ADQ92179
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Matches
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The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV0010-ABV62213) of the specification or its complement. (I) is useful for: (a) assessing whether proteiner is afflicted with prostate cancer; (b) monitoring the progression of prostate cancer; (b) monitoring the efficacy of a test compound to inhibit prostate cancer in a patient; (d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient; (e) assessing the prostate calc cancer in a patient; (f) assessing the prostate cell carcinogenic potential of a compound; (g) determining whether prostate cancer has metastasized in a patient; (d) assessing the aggressiveness or indolence of prostate cancer in a patient; (l) is also useful as a pharmacodyanamic or pharmacogenomic marker
                                                                                                                                                                                                                                  300
                    187
                                                                                        307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; prostate cancer; cytostatic; carcinogen; pharmacodyanamic marker; pharmacogenomic marker; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer.
                                                                                                                                                                                                                       241 GCATCTCTCGCTGGCTCAAACACGACAGTGTCCATTGGACAACAGAGAGTGGGAAT
68 AAGTGAAAAAGTGGAATGCAGTAGCCCTCTGGGCCTGGGATATTGTGGTTGATAACTGTG
                                                               CCATCTGCAGGAACCACATTATGGATCTTTGCATAGAATGTCAAGCTAACCAGGCGTCCG
                                                                                                                               CTACTTCAGAAGAGTGTACTGTCGCATGGGGAGTCTGTAACCATGCTTTTCACTTCCACT
                                                                                                                                                                cracricagaagagrgracrgrcgcarggggggrcrgraaccargcrrrrrcacrr
                                                                                                                                                                                                 GCATCTCTCGCTGGCTCAAAACACGCGGCTGTGTCCATTGGACAACAGAGAGTGGGAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human prostate expression marker cDNA 25606.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Page 5119-5120; 11750pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Monahan JE;
                                                                                                                                                                                                                                                                                                   301 rccaaaagrardeecacrae 320
                                                                                                                                                                                                                                                                   TCCAAAAGTATGGGCACTAG 327
                                                                                                                                                                                                                                                                                                                                                                                     ABV25615 standard; cDNA; 4476 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20-FEB-2001; 2001WO-US005171.
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2000US-0207454P.
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25-MAY-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                     ABV25615;
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Conservative

320;

Score 320; DB 12; Pred. No. 1.1e-98;

Length 503;

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CAGCGATGGATGTGGATACCCCGAGCGGCACCCAACACGGCGCGCGGCGAAGAAGCGCTTTG

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WO200177389-A2
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                                                                                                             CTTTGAAGTGAAAAAGTGGAATGCAGTAGCCCTCTGGGCCTGGGATATTGTGGTTGATAA 899
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                                                                                                                                                                                                                CCACTGCATCTCTCGCTGGCTCAAAACACGACAGGTGTGTCCATTGGACAACAGAGAGTG 302
                                                                                                                                                                                                                         CCACTGCATCTCTCGCTGCTCAAAACACGACGGGTGTCCATTGGACAACAGAGAGTG 719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to a purified nucleic acid molecule associated with
                                                               62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         and muscle and fat identification and analysis,
                                                                                                                                                                                                                                                                                                                                                                                             expressed sequence tag; lactation; LMFD; n; fat deposition; genome mapping; gene identification;
                                                                                                                                                 CTGTGCCATCTGCAGGAACCACATTATGGATCTTTGCATAGAATGTCAAGCTAACCAGGC
                                                                                                                                                                                       GTCCGCTACTTCAGAAGAGTGTACTGTCGCATGGGAGTCTGTAACCATGCTTTCACTT
                                                                               CTTTGAAGTGAAAAGTGGAATGCAGTAGCCCTCTGGGCCTGGGATATTGTGGTTGATAA
                                                                                                                                      CTGTGCCATCTGCAGGAACCACATTATGGATCTTTGCATAGAATGTCAAGCTAACCAGGC
                                                                                                                                                                            GTCCGCTACTTCAGAAGAGTGTACTGTCGCATGGGGAGTCTGTAACCATGCTTTTCACTT
                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                           Bovine BST associated with lactation/muscle/fat deposition #4677
       Sequence 4476 BP; 1085 A; 1129 C; 1015 G; 1247 T; 0 U; 0 Other;
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                          DB 5; Length 4476;
                                            IndelB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   deposition, useful for genome mapping, gene identific.
cattle breeding, or for genetically improving cattle.
                        Score 308.8; DB 5;
Pred. No. 2.2e-94;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Warren WC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New nucleic acid associated with lactation,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 2; SEQ ID NO 4677; 245pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tao N,
                                                                                                                                                                                                                                                                                                                     ABX39512 standard; cDNA; 380 BP
                                                                                                                                                                                                                                                                                                                                                                                                              gene analysis; cattle breeding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24-SEP-2001; 2001US-00960352.
                        Query Match 94.4%;
Best Local Similarity 99.4%;
Watches 310; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12-JAN-1999; 99US-0115707P.
                                                                                                                                                                                                                                                                                                                                                         20-FEB-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Byatt JC, Mathialagan N,
                                                                                                                                                                                                                                                     GGAATTCCAAAA 314
                                                                                                                                                                                                                                                                     GGAATTCCAAAA 707
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MATHIALAGAN N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2003-110599/10.
                                                                                                                                                                                                                                                                                                                                                                                             Bovine; ss; EST; ex
muscle deposition;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WARREN W C.
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                          Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62 AAGTGAAAAAGTGGAATGCAGTAGCCCTCTGGGCTGGGATATTGTGGTTGATAACTGTG 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          187
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         present sequence was not shown in the specification but was obtained in electronic format from the USPTO web site:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 CAGCGATGGATGTGGATACCCCGAGCGGCACCAACAGCGGGGGCGCGGCGAAGAAGCGCTTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    122 CCATCTGCAGGAACCACATTATGGATCTTTGCATAGAATGTCAAGGCGAACCAGGCGTCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GCATCTCTCGCTCGAAAACACGACAGGTGTGTCCATTGGACAACAGAGAGTGGGAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAGTGAAAAAGTGGAATGCAGTAGCCCTCTGGGCCTGGGATATTGTGGTTGATAACTGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CTACTTCAGAAGAGTGTACTGTCGCATGGGGAGTCTGTAACCATGCTTTTCACTTCCACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cractricidaagagigeacereecereeegegicigraacearecriticacritecacr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CCATCTGCAGGAACCACATTATGGATCTTTGCATAGAATGTCAAGCTAACCAGGCGTCCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human DNA sequence #99 expressed during foam cell differentiation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       92.5%; Score 302.4; DB 8; Length 380; 96.6%; Pred. No. 1e-92; tive 0; Mismatches 11; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 380 BP; 98 A; 87 C; 103 G; 92 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     segdata.uspto.gov/sequence.html?DocID=20020137139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TCCAAAAGTATGGGCACTAG 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           302 rccaaaggrangegcachag 321
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ilarity 96.6%;
Conservative
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Matches 309; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GCTTTGAAGTGAAAAGTGGAATGCAGTAGCCCTCTGGGCCTGGGATATTGTGGTTGATA 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                        61
                                                                                                                                                           Composition useful for diagnosis of conditions, disorders or diseases associated with atherosclerosis, comprises several polynucleotides that are differentially expressed in foam cell development.
                                                                                                                                                                                                                         The present invention relates to the isolation of human polynucleotide sequences that are differentially expressed during foam cell differentiation. The polynucleotide sequences of the invention or a composition comprising these polynucleotides are useful as a high throughput method for detecting altered expression of one or more polynucleotides in a sample. The polynucleotides can be used in the diagnosis of disorders associated with foam cell development such as atherosclerosis, cerebral stroke, and cardiovascular disorders such as coronary artery disease. The polynucleotide sequences can also be used both primers and probes. The polynucleotides of the invention are also useful in gene therapy. AAS94746-AAS59021 represent the human polynucleotide sequences of the invention which are differentially
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GCTTTGAAGTGAAAAGTGGAATGCAGTAGCCCTCTGGGCCTGGGATATTGTGTTTTGTATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACTGTGCCCATCTGCAGGAACCACATTATGGATCTTTGCATAGAATGTCAAGCTAACCAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CGTCCGCTACTTCAGAAGAGTGTACTGTCGCATGGGGAGTCTGTAACCATGCTTTTCACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TCCACTGCATCTCTCGCTGGCTCAAAACACGACAGGTGTGTCCATTGGACAACAGAGAGT
                                                                                                   Seilhamer JJ, Porter GJ, Mikita T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGCGGCAGCGATGGATGTGGATACCCCGAGCGCCACCAACAGCGGCGC-GGGCAAGAAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                  1;
                                                                                                                                                                                                                                                                                                                                                                                        Sequence 5347 BP; 1489 A; 1277 C; 1094 G; 1487 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                             DB 6; Length 5347;
                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
92.1%; Score 301.2; DB 6; Length
Best Local Similarity 98.7%; Pred. No. 9.4e-92;
Matches 314; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                 expressed during foam cell differentiation
                                                                                                                                                                                                         Claim 1; Page 151-152; 315pp; English.
                                                                                                      Lawn R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GGGAATTCCAAAAGTATG 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGGAATTCCAAAAGTAGG 202
                                    04-APR-2001; 2001WO-US011128.
                                                          05-APR-2000; 2000US-0195106P
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                                                                                                      Shiffman D, Somogyi R,
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diabetic; pre-diabetic; Type 2 diabetes; antidiabetic; gene therapy; diabetes; insulin resistance; metabolic disease; human; gene; ss.
Human Testican-1 nucleotide sequence SEQ ID NO:9.
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04-JUN-2002;
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META-) METABOLEX INC.

ΰ Wong Waters S, Moodie S, Lavan B, Gregoire F, Allan B,

WPI; 2004-053469/05. P-PSDB; ADF42704. Identifying an agent for treating diabetic or pre-diabetic individuals comprises contacting an agent with a polypeptide, e.g., human ceramidase, and selecting an agent that modulates the expression or activity of the polypeptide.

Disclosure; SEQ ID NO 9; 209pp; English

The present invention describes a method for identifying an agent for treating a diabetic or pre-diabetic individual. The method comprises contacting an agent to a mixture comprising a polypeptide encoded by a nucleic acid that hybridises under stringent conditions to a nucleic acid condition, and selecting an agent that modulates the expression or excivity of the polypeptide. Also described: (1) a method of treating a diabetic animal, comprising administering to the animal a comprising introducing an expression cassette into a cell, comprising introducing into the cell an expression cassette comprising a promoter operably linked to a polynucleotide encoding a polypeptide, where the polynucleotide hybridises under stringent conditions to a nucleic acid encoding the above amino acid sequences; and (3) a method of diagnosing an individual who has Type 2 diabetes or is pre-diabetic, comprising detecting in a sample from the individual the level of the above-mentioned polynucleotide encoding control or the polypeptide or the level of the above-mentioned polynucleotide encoding control or polynucleotide in the sample compared to a level of the polypeptide or conditions in diadrates that the individual is diabetic or pre-diabetic. The method is useful in diagnosing and treating diabetes, insulin resistance or related metabolic diseases in human subjects. The method may also be

ADF42703 standard; cDNA; 3484

(first entry)

26-FEB-2004

ADF42703;

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300 GCCCGCAGCGATGGATGTGGATACCCCGAGCGGCACCAACAACGAGCGGCGGGGAAGAAGAG 241
                                                                                                                                                                                                                 123 CTGTGCCATCTGCAGGAACCACATTATGGATCTTTGCATAGAATGTCAAGCTAAACCAGGC 182
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used in identifying agents for treating diabetic or pre-diabetic individuals. The present sequence is used in the exemplification of the present invention.
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                                                                                         Query Match
90.8%; Score 296.8; DB 12; Length 3484;
Best Local Similarity 99.3%; Pred. No. 2.4e-90;
Matches 298; Conservative 0; Mismatches 2; Indels 0;
                                                              Sequence 3484 BP; 894 A; 910 C; 808 G; 872 T; 0 U; 0 Other;
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Relatiing to Osteoarthritis
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Sequence 43377, Application US/10242535A; Publication No. US2004001363A1; Publication No. US2004001363A1; Publication No. US2004001363A1; Publication No. US2004001363A1
GENERAL INFORMATION:
APPLICANT: Chondrodene Inc.
TITLE OF INVENTION: Compositions and Methods Religible No. C.C.
TITLE OF INVENTION: Compositions and Methods Religible NETHING DATE: 2002-09-12; PRIOR APPLICATION NUMBER: US 10/085,783; PRIOR APPLICATION NUMBER: US 60/305,340; PRIOR FILING DATE: 2001-07-13; PRIOR PELING DATE: 2001-07-13; PRIOR FILING DATE: 2001-07-13; PRIOR FILING DATE: 2001-07-13; PRIOR FILING DATE: 2001-07-13; PRIOR FILING DATE: 2001-03-28; NUMBER: OF SEQ ID NOS: 58994; SOFTWARE: PATENTIN VERSION 3.2; SOFTWARE: VERSION 3.3; VERSI
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ORGANISM: Human
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- 2005 Compugen Ltd.
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Sequence 58211, A Sequence 19847, A Sequence 19847, A Sequence 46883, A Sequence 46883, A Sequence 46883, A

Sequence 50604, A Sequence 27, Appl Sequence 27, Appl Sequence 27, Appl Sequence 48516, A Sequence 48516, A Sequence 58211, A

Sequence 14771, A Sequence 2521, Ap Sequence 4357, Ap Sequence 687, App

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Sequence 35025 Application US/10242535A

Publication No. US20040013663A1

GENERAL INFORMATION:

APPLICANT: Chondrodene Inc.

APPLICANT: Chondrodene Inc.

TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis

FILE REPREMENT: 42005

CURRENT APPLICATION NUMBER: US/10/242,535A

CURRENT FILING DATE: 2002-09-12

PRIOR APPLICATION NUMBER: US 60/305,340

PRIOR FILING DATE: 2001-07-13

PRIOR FILING DATE: 2001-07-13

PRIOR FILING DATE: 2001-07-13

PRIOR FILING DATE: 2001-03-12

PRIOR FILING DATE: 2001-03-12

PRIOR FILING DATE: 2001-02-28

NUMBER OF SEQ ID NOS: 56994

SOFTWARE: PatentIn version 3.2

SEQ ID NO 35025
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Publication No. US20040037841A1
GENERAL INFORMATION:
APPLICANT: ChondroGene Inc.
TITLE OF INVENTION: Compositions and Methods Relatiing to Osteoarthritis
FILE REFERENCE: 4231/2002
CURRENT APPLICATION NUMBER: US/10/085,783A
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ORGANISM: Human
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Publication No. US20040037841A1

GENERAL INFORMATION:

APPLICANT: ChondroGene Inc.

APPLICANT: Liew, C.C.

TITLE OF INVENTION UNDER: US/10/085,783A

CURRENT APPLICATION NUMBER: US 60/305,340

PRIOR APPLICATION NUMBER: US 60/275,017

PRIOR APPLICATION NUMBER: US 60/275,017

PRIOR PILING DATE: 2001-07-13

PRIOR FILING DATE: 2001-07-13

PRIOR PILING DATE: 2001-07-13

PRIOR PILING DATE: 2001-07-13

PRIOR PILING DATE: 2001-07-13

PRIOR APPLICATION NUMBER: US 60/275,017

PRIOR APPLICATION NUMBER: US 60/271,955

PRIOR APPLICATION NUMBER: US 60/271,955
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                                                                 AACTGTGCCATCTGCAGGAACCACATTATGGATCTTTGCATAGAATGTCAAGCTAACCAG
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Matches 327; Conser
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US-10-085-783A-43377
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APPLICANT: Chondrodene Inc.
APPLICANT: Liew, C.C.
TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
FILE REFERENCE: 4231/2002
CURRENT APPLICATION NUMBER: US/10/085,783A
CURRENT FILING DATE: 2002-02-28
FRIOR PILING DATE: 2001-07-13
FRIOR PILING DATE: 2001-07-13
FRIOR FILING DATE: 2001-03-12
FRIOR FILING DATE: 2001-03-12
FRIOR FILING DATE: 2001-03-12
FRIOR FILING DATE: 2001-03-12
FRIOR FILING DATE: 2001-03-13
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           0; Indels
        0; Mismatches
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Publication No. US20040037841A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 100.
Matches 327; Conservative
        327; Conservative
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GENERAL INFORMATION:

APPLICANT: ChondroGene Inc.

APPLICANT: Liew, C.C.

TITLE OF INVENTION: Compositions and Methods Relatiing to Osteoarthritis
FILE REFRENCE: 4231/2005

CURRENT APPLICATION NUMBER: US/10/242,535A

CURRENT FILING DATE: 2002-09-12

PRIOR FILING DATE: 2001-07-13

PRIOR FILING DATE: 2001-07-13

PRIOR FILING DATE: 2001-07-13

PRIOR APPLICATION NUMBER: US 60/275,017

PRIOR FILING DATE: 2001-03-12

PRIOR FILING DATE: 2001-03-28

PRIOR FILING DATE: 2001-03-28

PRIOR FILING DATE: 2001-03-28

NUMBER: US 60/275,017
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                                                                                                                                                                                                                                                                                                                                                                                                                          Length 453;
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CURRENT FILING DATE: 2002-02-28
PRIOR APPLICATION NUMBER: US 60/305,340
PRIOR FILING DATE: 2001-07-13
PRIOR PILING DATE: 2001-07-15
PRIOR PILING DATE: 2001-03-12
PRIOR PILING DATE: 2001-03-28
PRIOR FILING DATE: 2001-02-28
NUMBER OF SEQ ID NOS: 58994
SOFTWARE: PALENTIN VERSION 3.2
SEQ ID NO 35025
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-242-535A-39933
; Sequence 39933, Application US/10242535A
; Publication No. US20040013663A1
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Best Local Similarity 100.
Matches 327; Conservative
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Best Local Similarity
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; ORGANISM: Human
US-10-085-783A-35025
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; ORGANISM: Human
US-10-242-535A-39933
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SEQ ID NO 39933
LENGTH: 467
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US-10-242-535A-56068
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; ORGANISM: Human
US-10-085-783A-57254
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Fublication No. US20040013663A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Chordrodene Inc.
APPLICANT: Chordrodene Inc.
TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
FILE REFRENCE: 4231/2005
CURRENT FILING DATE: 2002-09-12
PRIOR APPLICATION NUMBER: US 10/085, 783
PRIOR APPLICATION NUMBER: US 60/305, 340
PRIOR FILING DATE: 2001-07-13
PRIOR FILING DATE: 2001-07-13
PRIOR FILING DATE: 2001-03-12
SPRIOR PRIOR FILING DATE: 2001-03-12
SPRIOR DATE: 2001-03-12
SPRIOR DATE: 2001-03-12
SPRIOR DATE: 2001-03-12
SPRIOR DATE: 2001-03-12
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PUBLICATION No. US20040037841A1
GENERAL INFORMATION:
APPLICANT: ChondroGene Inc.
PAPPLICANT: Likew, C.C.
TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
FILE REPERENCE: 4231/2002
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100.0%; Score 327; DB 17; Length 471;
Best Local Similarity 100.0%; Pred. No. 4.2e-104;
Matches 327; Conservative 0; Mismatches 0; Indels 0
                                                                                            320 TGGGAATTCCAAAAGTATGGGCACTAG 346
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US-10-085-783A-57254
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US-10-242-535A-57254
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US-10-242-535A-56068

j. Sequence 56068, Application US/10242535A
j. Sequence 56068, Application No. US20040013663A1
general in No. US20040013663A1
general information:
APPLICANT: Chondrodene Inc.
APPLICANT: Chondrodene Inc.
TITLE OF INVENTION: Compositions and Methods Relatiing to Osteoarthritis
FILE REFERENCE: 4231/206
CURRENT APPLICATION NUMBER: US/10/242,535A
CURRENT FILING DATE: 2002-09-12
PRIOR APPLICATION NUMBER: US 60/305,783
PRIOR APPLICATION NUMBER: US 60/305,340
PRIOR FILING DATE: 2001-07-13
PRIOR APPLICATION NUMBER: US 60/275,017
PRIOR FILING DATE: 2001-02-28
NUMBER OF SEQ ID NOS: 58994
software: PatentIn version 3.2
LENGTH. 472
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100.0%; Pred. No. 4.2e-104;
tive 0; Mismatches 0;
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CURRENT APPLICATION NUMBER: US/10/085,783A
                      CURRENT FILING DATE: 2002-02-28
PRIOR APPLICATION NUMBER: US 60/305,340
PRIOR FILING DATE: 2001-07-13
PRIOR FILING DATE: 2001-03-12
PRIOR FILING DATE: 2001-03-12
PRIOR FILING DATE: 2001-03-8
PRIOR FILING DATE: 2001-03-8
NUMBER OF SEQ ID NOS: 58994
SOFTWARE: Patentin version 3.2
SEQ ID NO 57254
LENGTH: 471
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Best Local Similarity 100.0
Matches 327; Conservative
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ORGANISM: Human
FEATURE:
NAME/KEY: misc feature
LOCATION: (437)..(437)
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120

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sequence 3, Application US/10913937
sequence 3, Application US/10913937
sequence 3, Application No. US20050019813A1
sequence 3, Application No. US20050019813A1
sequence 3, Application No. US20050019813A1
septicant: Conaway, Ronald C.
APPLICANT: Conaway, Ronald C.
APPLICANT: Kamura, Takumi
APPLICANT: Kamura, Takumi
Septicant: Kamura, Takumi
Septicant: Kamura, Takumi
TITLE OF INVENTION: Novel Component of von Hippel-Lindau Tumor Suppressor
TITLE OF INVENTION: Complex and SCF Ubiquitin Ligase
TITLE OF INVENTION: Complex and SCF Ubiquitin Ligase
TITLE OF INVENTION: Complex us/10/913,937
CURRENT APPLICATION NUMBER: US/09/914,324
PRIOR FILING DATE: 2001-08-02
PRIOR APPLICATION NUMBER: US/09/914,324
PRIOR FILING DATE: 2000-02-26
PRIOR FILING DATE: 2000-02-25
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PatentIN Ver. 2.1
SEQ ID NO 3
LENGTH: 508
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Best Local Similarity 100.
Matches 327; Conservative
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; LOCATION: (7)..(333)
; OTHER INFORMATION: Rbx1
US-10-913-937-3
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US-10-913-937-3
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; PRUBLICATION NO. US20040037841A1
; GENERAL INFORMATION:
; APPLICANT: Chondarodene Inc.;
; APPLICANT: Chondarodene Inc.;
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; FILE REPREMENCE: 4231/2002
; CURRENT APPLICATION NUMBER: US /10/085, 783A
; CURRENT FILING DATE: 2001-02-28
; PRIOR PILING DATE: 2001-07-13
; PRIOR FILING DATE: 2001-07-13
; PRIOR FILING DATE: 2001-03-12
; PRIOR FILING DATE: 2001-03-12
; PRIOR PILING DATE: 2001-03-28
; NUMBER OF EXQ ID NOS: 58994
; SOFTWARE: PARENTIN VERSION 3.2
; ELENGTH: 472
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100.0%; Pred. No. 4.3e-104;
vative 0; Mismatches 0;
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100.0%; Pred. No. 4.3e-104;
ative 0; Mismatches 0;
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| NAME/KEY: misc feature
| LOCATION: (455)... (455)
| OTHER INFORMATION: n is a, c, US-10-085-783A-56068
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                                       NAME/KEY: misc_feature

LOCATION: (455)...(455)

CTHER INFORMATION: n is a,

US-10-242-555A-56068
OTHER INFORMATION: n is a,
                                                                                                                                                 Query Match
Best Local Similarity 100.
Matches 327; Conservative
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Best Local Similarity 100.
Matches 327; Conservative
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LOCATION: (437)...(437)
OTHER INFORMATION: n is
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US-10-085-783A-56068
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US-10-242-535A-46292
; Sequence 46292, Application US/10242535A
; Sequence 46292, Application No. US20040013663A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; APPLICANT: Liew, C.C.
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; PILE REFERENCE: 4231/2005
; CURRENT FILING DATE: 2002-09-12
; PRIOR FAPLICATION NUMBER: US 10/085,783
; PRIOR FILING DATE: 2002-09-12
; PRIOR FILING DATE: 2001-07-13
; PRIOR PAPLICATION NUMBER: US 60/275,017
; PRIOR PAPLICATION NUMBER: US 60/275,017
; PRIOR PELING DATE: 2001-07-13
; PRIOR PELING DATE: 2001-03-12
; PRIOR PELING DATE: 2001-03-12
; PRIOR SEQ ID NOS: 58994
; SOFTWARE: PRECENTIN VERSION 3.2
; TEMBER OF SEG ID NOS: 58994
; SOFTWARE: PRECENTIN VERSION 3.2
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                                                  241 TICCACTGCATCTCTCGCTGGCTCAAAACACGACAGGTGTGTCCATTGGACAACAGAGAG 300
                                                                     247 TTCCACTGCATCTCTCGCTGGCTCAAACACGACAGGTGTGTCCATTGGACAACAGAGA 306
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Matches 327; Conservative
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ORGANISM: Human
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US-10-085-783A-46292 ; Sequence 46292, Application US/10085783A ; Publication No. US20040037841A1

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APPLICANT: ChondroGene Inc.
APPLICANT: Liew, C.C.
TITLE OF INVENTION: Concestions and Methods Relatiing to Osteoarthritis
FILE REFERENCE: 4231/2002
CURRENT APPLICATION NUMBER: US/10/085,783A
CURRENT FILING DATE: 2001-02-28
PRIOR PRICATION NUMBER: US 60/305,340
PRIOR PILING DATE: 2001-07-13
PRIOR PILING DATE: 2001-03-12
PRIOR APPLICATION NUMBER: US 60/275,017
PRIOR FILING DATE: 2001-03-12
PRIOR PILING DATE: 2001-02-28
NUMBER OF SEQ ID NOS: 58994
SOFTWARE: Patentin version 3.2
LENGTH: 523
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publication No. US20030073623A1

GENERAL INFORMATION:
APPLICANT: Hyesq, Inc.
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
FILE REFERENCE: 20411-756

CURRENT APPLICATION NUMBER: US/09/918,995

CURRENT FILING DATE: 1201-07-30

PRIOR FILING DATE: 1999-01-20

NUMBER OF SEQ ID NOS: 38054

SOFTWARE: PSECENCE OF Windows Version 3.0

SEQ ID NO 17191
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LOCATION: (1)...(476)
OTHER INFORMATION: n = A,T,C or
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Matches 327; Conservative
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ORGANISM: Human
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                                                                       Length 476;
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99.4%; Score 325; DB 10; Length 47
Best Local Similarity 100.0%; Pred. No. 2.2e-103;
Matches 325; Conservative 0; Mismatches 0; Indels
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US-10-198-846-11311
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US-10-198-846-11311/c
US-09-918-995-17191
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Db 909 GTCCGCTACTTCAGAAGAGTGTACTGTCGCATGGGGAGTCTGTAACCATTTTCACTT 850

Qy 243 CCACTGCATCTCTCGCTGGCTCAAAACACGAGAGTCTGTAACCATGGACAACAGAGTGT

Db 849 CCACTGCATCTCTCGCTGGCTCAAAACACGACAGGTGTCCATTGGACAACAGAGTG 302

Qy 303 GGAATTCCAAAAGTATGGGCACTAG 327

Db 789 GGAATTCCAAAAGTATGGGCACTAG 327
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Search completed: June 24, 2005, 08:54:11 Job time: 1568 secs

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                                                                        June 24, 2005, 00:30:07; Search time 2179 Seconds (without alignments) 5712.261 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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                                                  OM nucleic - nucleic search, using sw model
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                 IDENTITY NUC Gapoxt 1.0
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327
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9b_est2::
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Perfect score:
                                                                                                                                                                                 Scoring table:
                                                                                                                                                                                                                       Searched:
                                                                                                                                                         Sequence:
                                                                                                                                                                                                                                                                                                                                                                    Database
                                                                            Run on:
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No.
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BU601080 AGENCOURT	BU954591 AGENCOURT	CD388268 AGENCOURT	CK003869 AGENCOURT	CD175085 AGENCOURT	BU861191 AGENCOURT	BUS97842 AGENCOURT	BUS33405 AGENCOURT	BP308845 BP308845	BP317451 BP317451	BG705958 602669278	BG503311 602550721	BU533420 AGENCOURT	BU959349 AGENCOURT	BG481544 602528456	BM459634 AGENCOURT	BQ216738 AGENCOURT	BQ050461 AGENCOURT	BG531117 602561424	BE738587 601572878	BF956282 QV2-NN004	•
5 BU601080	5 BU954591	Ŭ	7 CK003869	6 CD175085	5 BU861191	_	5 BU533405	5 BP308845	5 BP317451	4 BG705958	4 BG503311	5 BU533420	5 BU959349	4 BG481544	4 BM459634	5 BQ216738	5 BQ050461	4 BG531117	2 BE738587	4 BF956282	
555	557	558	559	562	563	570	573	581	583	616	736	801	845	988	904	945	1098	403	448	405	
100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	7.66	7.66	99.5	
327	327	327	327	327	327	327	327	327	327	327	327	327	327	327	327	327	327	326	326	325.4	
25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	C 44	45	

ALIGNMENTS

RESULT 1	
N305890	
OCUS	CN305890 462 bp mRNA linear EST 16-MAY-2004
DEFINITION	044616 GRN_PREHEP
CCESSION	
ERSION	CN305890.1 GI:47322304
CEYWORDS	
SOURCE	
ORGANISM	
	Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
	Primates;
REFERENCE	1 (bases 1 to 462)
AUTHORS	Brandenberger, R., Wei, H., Zhang, S., Lei, S., Murage, J., Fisk, G.J.,
	Li, Y., Xu, C., Fang, R., Guegler, K., Rao, M.S., Mandalam, R.,
	Lebkowski, J and Stanton, L.W.
TITLE	Transcriptome characterization elucidates signaling networks that
	control human ES cell growth and differentiation
JOURNAL	Nat. Biotechnol. 22 (6), 707-716 (2004)
COMMENT	Contact: Brandenberger R
	Regenerative Medicine
	Geron Corporation
	230 Constitution Drive, Menlo Park, CA 94025, USA
	Tel: 650 473 8658
	Fax: 650 473 7760
	Email: rbrandenberger@geron.com
	Insert Length: 462 Std Error: 0.00.
FATURES	Location/Oualifiers
Bource	1462
	/organism="Homo gapiens"
	/ CONTRACT CONTRACT
	יייייייייייייייייייייייייייייייייייייי
):
	1211C
	/Clone_lib="GKN_PKEHEP"
	1-length enriched cDNA II
	from DMSO-treated hES cell line H9 (p22) maintained in
	feeder-free conditions"
RIGIN	
Query Match	
,,,	Similarity 100.0%; Pred. No. 3.3e-91;
Matches 3	327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
£	1 ATGGCGGCAGCGATGGATGTGGATACCCCGAGCGGCACCAACAGCGGCGGGGGGAGAAG 60
Ď	23 ATGGCGGCAGCGATGGATGTGGATACCCCGAGCGGCACCAACAGCGGCGGGGCGCGGCAAGAAG

120

281

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/organism="Homo sapiens"
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/dlone lib="NIH MGC 21"
/dlone lib="NIH MGC 21"
/dlone lib="NIH MGC 21"
/dlone lib="nil" MGG 21"
/dlone
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Eukaryota; Matazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Butheria; Primates; Catarrhini; Hominidae; Homo.
E. 1 (bases I to 473)
Ebert, L., Heil, O., Hennig, S., Neubert, P., Partsch, E., Peters, M.,
Radelof, U., Schneider, D. and Korn, B.
Human Unigeneset - RZPD3
Contact: Ina Rolfs
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
IM Neuenhaimer Feld S80, D-69120 Heidelberg, Germany
RZPD; IMAG958P131435.
RZPDIIB; I.M.A.G.E. cDNA Clone Collection;
Human Unigeneset - RZPD3 (RZPDLIB No.972)
http://www.rzpd.de/CloneCards/cgi-
bin/showlib.pl.cgi/response?libNo-972 Contact: Ina Rolfs
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Heubnerweg 6, D-14059 Berlin, Germany
Tel: +49 30 32639 111
Fax: +49 30 32639 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BX283972 BX283972 Homo sapiens cDNA clone IMAGp958P131435 ; IMAGE:4652028, mRNA sequence.
121 AACTGTGCCATCTGCAGGAACCACATTATGGATCTTTGCATAGAATGTCAAGCTAACCAG 180
                                                                                                                                                                                                                                                                                                                                                                162 AACTGTGCCATCTGCAGGAACCACATTATGGATCTTTGCATAGAATGTCAAGCTAACCAG 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GCGTCCGCTACTTCAGAAGAGTGTACTGTCGCATGGGGAGTCTGTAACCATGCTTTTCAC 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             241 TTCCACTGCATCTCTCGCTGGCTCAAACACGACAGGTGTGTCCATTGGACAACAGAGAG 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      282 TTCCACTGCATCTCTCGCTGGCTCAAAACACGACAGGTGTGTCCATTGGACAACAGAGAG 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This clone is available royalty-free from RZPD; contact RZPD (clone@rzpd.de) for further information. Seq primer: pCMV-M13u, Primer sequence: CGTTGTAAAACGACGGCCAGT. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       222 GCGTCCGCTACTTCAGAAGAGTGTACTGTCGCATGGGGAGTCTGTAACCATGCTTTTCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         301 TGGGAATTCCAAAAGTATGGGCACTAG 327
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Homo sapiens
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KEYWORDS
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/clone="IndexCollaborations"
/tissue_type="leiomyosarcoma cell line"
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/clone lib="NIH MGC 46"
/clone lib="NIH MGC 46"
/clone lib="NIH MGC 46"
/clone lib="ONA made by oligo-dT priming. Directionally cloned into EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI; cDNA constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley)
using ZAP-cDNA synthesis kit (Stratagene) and Superscript library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

E. 1 (bases 1 to 471)

E. 1 (bases 1 to 471)

I. Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Preparation: Ling Hong/Rubin Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Preparation: Library

CDNA Library Pr
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                                                               83 CGCTTTGAAGTGAAAAGTGGAATGCAGTAGCCCTCTGGGCCTGGGATATTGTGGTTGAT 142
                                                                                                                                                                                         AACTGTGCCATCTGCAGGAACCACATTATGGATCTTTGCATAGAATGTCAAGCTAACCAG 180
                                                                                                                                                                                                                             143 AACTGTGCCATCTGCAGGAACCACATTATGGATCTTTGCATAGAATGTCAAGCTAACCAG 202
                                                                                                                                                                                                                                                                                                                                                                GCGTCCGCTACTTCAGAAGAGTGTACTGTCGCATGGGGAGTCTGTAACCATGCTTTTCAC 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TTCCACTGCATCTCGCTGGCTCAAAACACGACAGGTGTGTCCATTGGACAACAGAGAG 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BG339057 471 bp mRNA linear EST 27-FEB-20
602436882F1 NIH_MGC_46 Homo sapiens CDNA clone IMAGE:4554597 5',
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     323 TGGGAATTCCAAAAGTATGGGCACTAG 349
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BG339057.1 GI:13145495
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Homo sapiens
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LOCUS DEFINITION

RESULT 2 BG339057

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ACCESSION VERSION KEYWORDS SOURCE

ORGANISM

REFERENCE AUTHORS TITLE JOURNAL

COMMENT

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FEATURES

1 ATGCCGCCAGCGATGGATGTGGATACCCCGAGCGGCACCAACAGCGGCGCGGCCAAGAAG 60

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ORIGIN

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    adaptor sequence:
    -ATTCTAGAGGCCGAGGGCCGACATG-dT(30)BN-3'

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Pan troglodytes
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                                                                                                                                                                                                                                                                                                   Best Local Similarity 100.
Matches 327; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1. .498
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/clone="lMAGE:4804661"
/tissue type="adenocarcinoma"
/lab_host="DH10B (T1 phage-resistant)"
/clone lib="NHH MGC 60"
/hote="Corgan: prostate; Vector: pDNR-LIB (Clontech);
Site_1: Sfil (ggcgcctcggcc); Site_2: Sfil
(ggccattatggcc); Double-stranded cDNA was prepared from cell line RNA. 5' and 3' adaptors were used in cloning as fall and an adaptors were used in cloning as fall control of the control of the
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602664820F1 NIH_MGC_60 Homo sapiens cDNA clone IMAGE:4804661 5',
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(Stratagene) and Superscript II RT (Life Technologies)."
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 488)
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Email: cgapbe-remail.nih.gov
Tissue Procurement: DCTD/DTP
CDNA Library Preparation: CLONETECH Laboratories, Inc.
CDNA Library Preparation: CLONETECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.lln.gov
Plate: LLCM1651 row: h column: 06
High quality sequence stop: 487.
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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                                                                                       Length 473;
                                                                                                                                            Indels
                                                                                 Query Match
100.0%; Score 327; DB 5;
Best Local Similarity 100.0%; Pred. No. 3.4e-91;
Matches 327; Conservative 0; Mismatches 0;
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/mol_type="mRNA"
/db_xref="taxon:9606"
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BG777485
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                            ORIGIN
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C, or G and N = A, C, G, or T). Average insert size 1.5 kb (range 0.9-4.0 kb). 14/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH MGC Library."
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
1 (bases 1 to 498)
Hellmann, I., Zollner, S., Enard, W., Ebersberger, I., Nickel, B. and
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12B22006_rev 1 C10 r 082.abl Chimpanzee brain library Koos Pan
troglodytes cDNA clone 12B22006_rev_1_C10_r_082.abl 5', mRNA
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Evolutionary Genetics

Max-Planck-Institute for evolutionary Anthropology
Deutscher Platz 6, 04103 Leipzig, Germany
Tel: +49-(0)-341-3550 500
Fax: +49-(0)-341-3550 555
Email: paabo@eva.mpg.de
Seg primer: M13 reverse.
Location/Qualifiers
                                                                                                                                                                                                                              100.0%; Score 327; DB 4; Length 488; 100.0%; Pred. No. 3.4e-91; ive 0; Mismatches 0; Indels
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/mol_type="mRNA"
/db_xref="taxon:9598"
/clone="12B22006_rev_1_C10_r_082.ab1"
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                                                                                                                Query Match 100.0%; Score 327; DB 7; Best Local Similarity 100.0%; Pred. No. 3.4e-91; Matches 327; Conservative 0; Mismatches 0;
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/organism="Homo sapiens"
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/db_Xref="taxon:9606"
/dov stage="adult"
/lab_host="DH10B"
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AL711573.1 GI:19694928
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/dev_stage="adult"
/lab_host="Epicurian Coli (TW) XL-10-Gold"
/clone_lib="Chimpanzee brain library Koos"
/note="Vector: pUChi; Site 1: Sfir-A; Site 2: Sfir-B; The library was prepared using the SMART cDNA Tibrary construction Kit (Clonecch), doing only primer extension, but not FOR amplification of the CDNA. The only deviation from the published protocoll was that we cloned the cDNA into a plasmid Vector."
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Contact: Brandenberger R
Regenerative Medicine
Geron Corporation
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

    (bases 1 to 509)

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                                                                                                                                                                                                                                                      /mol_type="mRNA" -
/db_xref="texon:9606"
/tisbuc_type="embryonic stem cell, retinoic acid and
mitogen-treated hBS cell line H7"
                                                                                                                                                                                                                         Gaps
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Li, Y., Xu, C., Fang, R., Guegler, K., Rao, M.S., Mandalam, R.,
Lebkowski, J and Stanton, L.W.
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                                                                                                                                                                                      Length 498;
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Tel: 650 473 8658
Email: rbrandenberger@geron.com
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                                                                                                                                                                                       100.0%; Score 327; DB 6; 100.0%; Pred. No. 3.4e-91;
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Location/Qualifiers
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17000600185586 GRN_PRENEU Homo
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/clone lib="GRN_PRENEU"
/note="Oligo dT primed, full-length enriched cDNA library
from hES cell line H7 (p29) maintained in feeder-free
conditions. Embryoid bodies were generated in the presence
of all-trans retinoic and mitogens."
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DKFZp686I0483 rl 686 (synonym: hlcc3) Homo sapiens cDNA clone
DKFZp686I0483 5', mRNA sequence.
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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Genome Project.
No sl sequence available.
This clone (DKRZp68610483) is available at the RZPD in Berlin.
This clone (DKRZp68610483) is sourcenzentrum, Heubnerweg 6, 14059
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
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This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKE3); Email s.wiemann@dkfz- heidelberg.de;
sequenced by BMF2 (Blomedical Research Center at the Charite,
Berlin/Germany) within the cDNA sequencing consortium of the Ge
                                                                                                                                                                                                                                                                                                                                                                181 GCGICCGCTACTICAGAAGAGTGTACTGTCGCATGGGGAGTCTGTAACCATGCTTTTCAC
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/organism="Homo sapiens"
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Matches 327; Conservative
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B. 1 (bases 1 to 525)

B. 1 (bases 1 to 525)

S. NIH-MGC http://mgc.nci.nih.gov/.

I. Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

Clone distribution: MGC clone distribution information can be http://image.llnl.gov

Plate: LLCM1250 row: e column: 01

High quality sequence stops: 525.
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/tissue_type="leiomyosarcoma cell line"
/tish host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_46"
/note="Organ: uterus; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor:
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/clone_lib="686 (synonym: hlcc3)"
/note="Vector: pTriplEx2; Site_1: SfiIA; Site_2: SfiIB;
cDNA-collection"
                                                                                                                                                                                                                                                                                                                                                 141 AACTGTGCCATCTGCAGGAACCATTATGGATCTTTGCATAGAATGTCAAGCTAACCAG
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6024350011 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4553064 5'
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                                                                                            100.0%; Score 327; DB 1;
100.0%; Pred. No. 3.4e-91;
ive 0; Mismatches 0;
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/organism="Homo sapiens"
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/db_xref="taxon:9606"
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GGCACCAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."
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University of Iowa
375 Newton Road, 4156 MEBRP, Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Bmail: bento.soares@ulowa.edu
cDNA Library preparation: Dr. M. Bento Soares, Univeristy of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa
DNA Sequencing by: Dr. M. Bento Soares, Univeristy of Iowa
Clone Distribution: Researchers may obtain clones from Research
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1 (basea 1 to 527)

Bonaldo, M.F., Lennon, G. and Soares, M.B.

Normalization and subtraction: two approaches to facilitate gene
                                                                                                                                                                                                                                                                                                                                                                                                                                               67 CGCTTTGAAGTGAAAAGTGGAATGCAGTAGCCCTCTGGGCCTGGGGATATTGTGGTTGAT
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100.0%; Pred. No. 3.4e-91;
ive 0; Mismatches 0; Indels
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Seq primer: M13 Reverse.
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cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can lfound through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov.e.column: 17 Plate: LLCM2955 row: e column: 17 High quality sequence stop: 498.

High quality sequence stop: 498.
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/organism="Homo sapiens"
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                                                                                                                                                                                                                              /mol_type="mRNA"
/db_xref="taxon:9606"
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Matches 327; Conservative
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                                                                                                                                    /done lib="UT-B-CLI"
//done lib="UT-B-CLI"
//done lib="UT-B-CLI"
//note="Organ: eye; Vector: pT/T3-Pac (Pharmacia) with a modified polylinker; Site 1: EccR i; Site 2: Not I; UT-B-CLI is a normalized CDNA library containing the following tissue (a): retina. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand CDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT/T3-Pac vector. The oligonoucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is CGGCG. This library was created for the program, Gene Discovery in the Visual System, supported by National Eye Institute (NEI)."
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1. (bages 1 to 527)
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AGENCOURT 10473929 NIH_MGC_127 Homo sapiens cDNA clone IMAGE:6673337 5', mRNA sequence.
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/lab_host="DH10B (Life Technologies)
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100.0%; Pred. No. 3.4e-91;
tive 0; Mismatches 0;
                                    db xréf="taxon:9606"
/clone="UI-E-CL1-afi-h-19-0-UI"
/tissue_type="human retina"
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: NCI
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         /doce=TMAGE:302649"
/lab_host=TMAGE:302649"
/lab_host="DH10B (T1 phage-resistant)"
/clone lib="NHH MGC 186"
/clone lib="NHH MGC 186"
/note=Togan: Polod-Skin; Vector: pDNR-LIB; Site 1: Sfil (ggccattatggce); Library is oligo-dT primed and directionally cloned. CDNA was prepared from a pooled samples of tissues from Skin, meninges, duramatter, pia matter and choroid plexus.
and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGGCCATATGCCC-3' and 3' adaptor sequence: 5'-CACGGCCAGGGCGCCC-3' and 3' adaptor sequence: 5'-CACGGCCCAGGGCGCCCC-3' and 3' adaptor sequence: 5'-CACGGCCCAGGCGCCCCC-3' and 3' adaptor sequence: 147 kb (range 0.50-4.0 kb). 15/15 colonies insert size 1.47 kb (range 0.50-4.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Liboratories (Palo Alto, CA). Note: this is a NIH_MGC
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/db_xref="taxon:9606"
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/ clone lib="SINU-5"
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/ clone add pyrophosphatase (TAP). The decapped
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Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R., Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and Kim,Y.S.
21C Frontier Korean BST Project 2001
Unpublished (2002)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Korea Research Institute of Bioscience & Biotechnology
52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
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Fax: +82-42-860-6409
Fight: 29 row: H column: 12
High quality sequence stop: 529.
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/db_xref="taxon:9606"
/clone="S1SNU5-29-H12"
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                                                                                                                                                                                                                                                                               Homo sapiens (human)
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Contact: Daniels S. Gerhard, Ph.D.

Office of Cancer Genomics
National Cancer Institute / NIH

Bldg. 31 Rm10A07 Betheads, MD 20892

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Narayan Bhat
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioceience Corporation
Clone distribution: MG.C. Clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: NDCM205 row: c column: 07

High quality sequence stop: 518.
       213 GCGTCCGCTACTTCAGAAGAGTGTACTGTCGCATGGGGAGTCTGTAACCATGCTTTTCAC 272
                                                                             241 TICCACTGCATCTCTCGCTGGCTCAAAACACGACAGGTGTGTCCATTGGACAACAGAGAG 300
                                                                                                                273 TTCCACTGCATCTCTCGCTGGCTCAAACACGACAGGTGTGTCCATTGGACAACAGAGAG 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria, Primates; Catarrhini; Hominidae; Homo.

(Dases 1 to 531)

NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cloning as follows: 5' adaptor sequence:
5'-CACGCCATTATGCCC-3' and 3' adaptor sequence:
5'-TTCTAGAGGCGCGACATG-dT(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.69 kb (range 0.70-5.0 kb). 15/15 colonies contained inserts and was constructed by Clontech laboratories (Palo Alto, CA). Note: this is a NIH_MGC Library."
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                                                                                                                                                                                                                                                                                                                                                                                                                                            CD523457
AGENCOURT 14360071 NIH MGC 191 Homo sapiens cDNA clone
IMAGE:30412182 5', mRNA sequence.
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/mol_type="mRNA"
//db_xref="taxon:9606"
/clone="UI=E-CKI-dif-h-19-0-UI"
/tissue_type="Retina Foveal and Macular"
/dev_stage="adult"
/dev_stage="adult"
/dev_stage="adult"
/dev_stage="adult"
/dev_stage="adult"
/dev_stage="adult"
/done lib="UI-B-CKI"
/clone lib="UI-B-CKI"
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Tissue Procurement: Dr. Gregg Hageman
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com).
Seq primer: M13 FORWARD
POLYA-YES.
                                                                                                                                                      180
                                                                                                                                                                                                                      GCGTCCGCTACTTCAGAAGAGTGTACTGTCGCGATGCGGAGTCTGTAACCATGCTTTTCAC 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         203 GCGTCCGCTACTTCAGAAGAGTGTACTGTCGCATGGGGAGTCTCTAACCATGCTTTTCAC 262
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                                                                                                                                                      121 AACTGTGCCATCTGCAGGAACCACATTATGGATCTTTGCATAGAATGTCAAGCTAACCAG
BU729963
UI-E-CK1-afi-h-19-0-UI.sl UI-E-CK1 Homo sapiens cDNA clone
UI-E-CK1-afi-h-19-0-UI 3', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Soares, MB Coordinated Laboratory for Computational Genomics
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to an ECOR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library as GTC. This library was created for the program, Gene Discovery in the Visual System, supported by National Eye Institute (NEI).

TAG INSUB-Foveal and Macular Retina TAG LIB-UI-E-CK1
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1 (Dases 1 to 537)
NIH-MGC http://mgc.nci.nih.gov/.
NIH-MGC http://mgc.nci.nih.gov/.
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BG478622 537 bp mRNA linear EST 21-MAR-2 602525509F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:4643619 5',
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Tissue Procurement: ATCC/DCTP/DTP
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1414 row: b column: 04
High quality sequence stop: 534.
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                                                                                                                                                                                                                                                                                                   Length 533;
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100.0%; Pred. No. 3.5e-91;
tive 0; Mismatches 0;
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Homo sapiens
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/tissue_type="melanotic melanoma"
/lab host="bH10B (phage-resistant)"
/clone_lib="NH1 MGC_20"
/cloned into BcoR1/Kh0; Vector: pOTB7; Site_1: Xho1; Site_2: BcoR1; cDNA made by oligo-dT priming. Directionally
/cloned into BcoR1/Kh0 Size-selected >S00bp for average adaptor: GGCACGG(G). Size-selected >S00bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using Zab-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
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Best Local Similarity 100.0%; Pred. No. 3.5e-91;
Matches 327; Conservative 0; Mismatches 0;
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Job time : 2188 secs
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Title: Perfect score:

Sequence:

OM protein -

Run on:

Scoring table:

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CQ712328 Sequence
CQ71142 Sequence
AX888031 Sequence
BD027641 Sequence
BD271522 VonHippel
AF140599 Mus muscu
CQ728899 Sequence
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AF140598 Homo Sapi
BC082183 Xenopus 1
CQ701366 Sequence
BC051473 Mus muscu
BC001466 Homo Sapi
BC017370 Homo Sapi
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BC017370 Homo Sapi
BC05692 Mus muscu
BC05692 Mus muscu
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BC081497 Danio rer
AC112970 Mus muscu
AC12970 Mus muscu
CQ709925 Sequence
CQ493737 Sequence
CQ493737 Sequence
AF085906 Homo sapi
AX281690 Sequence
X73608 H. sapiens m
AX281690 Sequence
X73608 H. sapiens m
AX192360 Sequence
CQ603273 Sequence
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AX118519 Ciona int
BT116119 Ciona int
AX118792 Oryza sat
AX092287 Oryza sat
AX09287 Oryza sat
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AX032066 Populus t
AX032331 Arabidops
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1 (bases 1 to 327)
Ohta, T., Michel, J.J., Schottelius, A.J. and Xiong, Y.
ROCI, a homolog of APC11, represents a family of cullin partners with an associated ubiquitin ligase activity
Mol. Cell 3 (4), 535-541 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (10-APR-1999) Lineberger Comprehensive Cancer Center, University of North Carolina at Chapel Hill, Mason Farm Rd. and Manning Dr., Chapel Hill, NC 27599-7295, USA Location/Qualifiers
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Homo sapiens RING finger protein
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BC081497
AC112970
AY027936
CC709825
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CC993137
AY281690
HSTEST
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Ohta,T., Michel,J. and Xiong,Y.
Direct Submission
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CR456560
BC017370
BC056992
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   Command line parameters:
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-MODEL=frame+ p2n.model - DEV=x1h
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-Q=/cgn2_1/USFVO_spool/US09541462_mbmand0.cdi -LIST=45
-UNITS=bits -START=1 - END=-1 -MATRIX=blosum62 - TRANS=bumand0.cdi -LIST=45
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-NO MAAP - LARGEQUER*Y - NGG SCORES=0 - WALT - DESPELOCK=100 - LONGIAG
- DEV TIMEOUT=120 - WARN TIMEOUT=30 - THEABS-1 - XGAPOP=10 - XGAPORT=0.5 - FGAPOP=6
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CQ698451 Sequence
CQ690099 Sequence
CQ695007 Sequence
                                                                                                                       ; Search time 1372 Seconds
  (without alignments)
1551.946 Million cell updates/sec
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                                                                                                                                                                                                                                 MAAAMDVDTPSGTNSGAGKK......KTRQVCPLDNREWEFQKYGH 108
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                    GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                     nucleic search, using frame_plus_p2n model
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Maximum Match 100%
Listing first 45 summaries
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CQ690099
CQ695007
                                                                                                                          June 24, 2005, 06:37:52
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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Maximum DB seq length: 200000000
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Compositions and methods relating to osteoarthritis
Patent: WO 02070737-A 35025 12-SEP-2002;
Chondrogene Inc. (CA)
Location/Qualifiers
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Sequence 35025 from Patent W002070737.
CQ690099.1 GI:42225827

    .453
    /organism="Homo sapiens"
    /mol_type="unassigned DNA"
    /db_xref="taxon:9606"

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Best Local Similarity:
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Best Local Similarity:
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Compositions and methods relating to osteoarthritis
Parent: WO 02070737-A 43377 12-SEP-2002;
Chondrogene Inc. (CA)
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RESULT 5 CQ712328 LOCUS CQ712328 CQ7123	Chondrogene Inc. (CA) FEATURES Location/Qualifiers 1 - 471 /organism="Homo sapiens" /mol_type="unassigned DNA" /db_xref="taxon:9606" Alignment Scores: Pred. No.: 616.00 Matches: 108 Bertcent Similarity: 100.00\$ Mismatches: 0 Best Local Similarity: 100.00\$ Mismatches: 0 DB: 6 Gaps: 0 INS-09-541-4629-2 (1-108) x CO712328 (1-471)		Qy 61 AlaSerAlaThrSerGluGluCysThrValAlaTrpGlyValCysAsnHisAlaPheHis 80 IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	SILT 6 711142 711142 711142 711142 711143 71143 71143 71143
Db 84 CGCTTTGAAGTGAAAAGTAGGAATGCAGTAGCCCTCTGGGCTGGGATATTGTGGTTGAT 143	RESULT 4 C0695007 LOCUS LOCUS LOCUS C0695007 C0696008 C06	FEATURES CHOMINGORN LOCATION (AA) FEATURES 1. 4670 (Qualifiers 1. 467) Source /organism=Homo sapiens" / 467 / 46	Gaps: Gaps	41 AsnCysAlaileCysArgAsnHisileMetAspleuCysIleGluCysGlnalaAsnGln 60 41 AsnCysAlaileCysArgAsnHisileMetAspleuCysIleGluCysGlnalaAsnGln 60 41 AstTGTGCCATTTGCAGGAACCATTTTTGCATTGCATAGAATTTAGGATTTTTGCATGGAATTTAGGATTTTTGCATGGAATTTAGGATTTTTGCATGAGAATTTAGGTTAACCAGGTTAACCAGGTTAACCAGGTTAACCAGGTTAACCAGGTTAACCAGGTTAACCAGGTTAACCATTTTCAC 25 41 PheHisCysIleSerArgTrpLeuLysThrArgGlnValCysProLeuAspAsnArgGlu 10 41

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PAT 27-AUG-2002
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1 (bases 1 to 482)
Sedwards, J.B.D.M., Duclair, E. and Jordan, J.Y.
Sequence tag and encoded human protein
Patent: JP 2001269182-A 3887 02-OCT-2001;
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JP 2001269182-A/3887
02-OCT-2001
24-FEB-2000 JP 2000118773
26-FEB-1999 US 60/122487
JGRN BAPUTIST DUMAS MILNE EDWARDS, EIMERIC DUCLAIR, JEAN YVES
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human protein.
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JP 2001269182-A/3887.
Homo sapiens (human)
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FQKYGH"
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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/note="unnamed protein product"
Patent: WO 02070737-A 56068 12-SEP-2002;
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Sequence 3894 from Patent EP1033401.
AX888031 GI:40046785
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AF140599 504 bp mRNA linear ROD 11-MAY-1999
Mus musculus ring-box protein 1 (Rbx1) mRNA, complete cds.
AF140599.1 GI:4769005
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Kamura, T., Koepp, D.M., Conrad, M.N., Skowyra, D., Moreland, R.J., Iliopoulos, O., Lane, W.S., Kaelin, W.G. Jr., Elledge, S.J., Conaway, R.C., Harper, J.W. and Conaway, J.W.

Rbxl, a component of the VHL tumor suppressor complex and SCF ubiquitin ligase.
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Kamura, T., Lane, W.S., Conaway, R.C. and Conaway, J.W.
Direct Submission
Submitted (OS-APR-1999) Prog. Molec. Cell Biol., HHMI, Oklaho
Med. Res. Fdn., 825 NE 13th St, Oklahoma City, OK 73104, USA
Location/Qualifiers
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            /db_xref="taxon:10095"
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E (bases I to 504)

S (conaway,J.W., Conaway,R.C. and Kamura,T.

VonHippel-Lindau tumor supressor complex and novel component of SCP ubiquitin ligase

L Patent. JP 2002541775-A 3 10-DEC-2002;

OKLAHOMA MEDICAL RESEARCH FOUNDATION
OS Mus sp. (murine)
PN JP 2002541775-A)
PD 10-DEC-2002
PF 25-FEB-2000 JP 2000601023
PR 26-FEB-1999 US 60/121787
PI JOAN W CONAWAY,RONALD C CONAWAY,TAKUMI KAMURA PC
CL2NIS/09,A6IK38/00,A6IK38/53,A6IK45/00,A6IP35/00,CO7K14/47, PC
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BD271522
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/organism="Mus sp."
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
In (Dases) 1 to 508)
Conaway, J.W.; Conaway, R.C. and Kamura, T.
VonHippel-Lindau tumor suppressor complex and novel component of SCF ubiquitin ligase
L. Patent: JP 200244175-A 1 10-DEC-2002;
OKLAHOMA WEDICAL RESERRCH FOUNDATION
OS Homo sapiens (human)
PN JP 2002441775-A/1
PP 10-DEC-2002
PF 25-FEB-2000 JP 2000601023
PR 25-FEB-2000 JP 2000601023
PR 25-FEB-2000 JP 200121787
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VonHippel-Lindau tumor suppressor complex and novel component of
SCF ubiquitin ligase.
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C12N1/19,C12N1/21,C12N5/10,C12N9/00,C12P21/02,G01N33/15,G01N33/
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PD 10-DEC-2002
PF 25-FEB-2000 JP 2000601023
PR 26-FEB-1999 US 60/121787
PI JOAN W CONAMAY, RONALD C CONAWAY, TAKUMI KAMURA PC CILNIS/09, AGIK38/00, AGIK38/53, AGIK45/00, AGIP35/00, CO7K14/47, CI2N1/15,
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product="ring-box protein 1"
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|db_xref="G1:4769006"
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Kits, such as nucleic acid arrays, comprising a majority of
humanexons or transcripts, for detecting expression and other uses
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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PE Corporation (NY) (US)
Location/Qualifiers
1. .507
/organism="Homo sapiens"
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Sequence 15833 from Patent WO02068579.
CQ728899 CQ729899.1 GI:42302243
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Homo sapiens ring-box protein 1 (RBX1) mRNA, complete cds.
AF140598
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

Kamura, T., Koepp, D.M., Conrad, M.N., Skowyra, D., Moreland, R.J.,

Iliopoulos, O., Lane, W.S., Kaelin, W.G. Jr., Elledge, S.J.,

Conaway, R.C., Harper, J.W. and Conaway, J.W.

Rbxl, a component of the VHL tumor suppressor complex and SCF

ubiquitin ligaes

Science 284 (5414), 657-661 (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (05-APR-1999) Prog. Molec. Cell Biol., HHMI, Oklahoma Med. Res. Pdn., 825 NE 13th St, Oklahoma City, OK 73104, USA Location/Qualifiers
                                                                                                                                             1 MetalaalaalametaspValaspThrProSerGlyThrAsnSerGlyAlaGlyLysLys
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Kamura, T., Lane, W.S., Conaway, R.C. and Conaway, J.W.
Direct Submission
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Strausberg, R. L., Feingold, E. A., Grouse, L. H., Derge, J. G., Klausner, R. D., Collins, F. S., Wagner, L., Shenmen, C. M., Schuler, G. D., Altschul, S. F., Zoeberg, B., Buetow, K. H., Schaefer, C. F., Bhat, N. K., Hopkins, R. F., Jordan, H., Moore, T., Max, S. I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G. M., Hong, L., Stapleton, M., Soares, M. B., Bonaldo, M. F., Casavant, T. L., Scheetz, T. E., Brownstein, M. J., Usdin, T. B., Toshiyuki, S., Carninoi, P., Prange, C., Raha, S.S., Loquellano, N. A., Peters, G. J., McKernan, R. J., Mullahy, S. J., Ganzian, P. H., Richards, S., McKernan, K. J., Malek, J. A., Ganzia, R. H., Richards, S., Wolley, K. C., Hale, S., Garcia, A.M., Gay, L. J., Hulyk, S. W., Villalon, D. K., Wuzny, D. M., Sodergren, B. J., Lu, X., Gibbs, R. A., Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
/translation="MaaamDVDTPSGTNSGACKKRFEVKKWAVALWAWDIVVDNCAI
CRNHIMDLCIECQANQASATSEECTVAWGVCNHAFHFHCISRWLKTRQVCPLDNREWE
FQKYGH"
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Xenopus laevis cDNA clone MGC:98645 IMAGE:7200307, complete cds.
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Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae;
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Klein, S.L., Strausberg, R.L., Wagner, L., Pontius, J., Clifton, S.W. and Richardson, P.
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Xenopus laevis
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PAT 03-FEB-2004
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                                                        AlaSerAlaThrSerGluGluCysThrValAlaTrpGlyValCysAsnHisAlaPheHis
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo
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Compositions and methods relating to osteoarthritis
Patent: WO 02070737-A 46292 12-SEP-2002;
Chondrogene Inc. (CA)
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Sequence 46292 from Patent W002070737.
CQ701366 GI:42262133
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/mol_type="unassigned DNA"
/db xrefe"taxon:9606"
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                                                                                                                                                   Klein, S. and Gerhard, D.S.
Klein, S. and Gerhard, D.S.
Direct Submission
Submitted (01-SEP-2004) National Institutes of Health, Xenopus Gene Collection (XGC), National Institute of Child Health and Human
Development, 6100 Executive Boulevard, Room 4B01, Rockville, MD
20892-7510, USA
                                                                                                                                                                                                                                                                                                    Contact: XGC help desk
Email: cgapbs-r@mail.nih.gov
Tissaue Procurement: Dr. Igor Dawid
Tissaue Procurement: Dr. Igor Dawid
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford, CA 94305
Web site: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: http://image.llnl.gov Series: IRAK Plate: 189 Row: f Column: 1 This clone was selected for full length sequencing because it passed the following selection criteria: Similarity but not
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/product=buhknown (protein for MGC:98645)"
/product=buhknown (protein for MGC:98645)"
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                                                                                                human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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/tissue_type="Embryo, stage 17/19, Xenopus"
/clone_lib="MICHD XGC_Embry
/lab hose="BH108"
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Search completed: June 24, 2005, 09:58:04 Job time : 3379 secs

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/*tag= a
/product= "ROC1"
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-Q=/cgn2_1/USPTO spool/US09541462/runat_23062005_122623_9472/app_query.fasta_1.263
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-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THRADS=1 -XGAPOP=10 -XGAPORT=0.5 -FGAPOP=6
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Aaa74980 DNA encod
Aq87496 Human tum
Adg87156 Human tum
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              GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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                                                                                                                                             The present sequence encodes a human ROC1 ring finger protein. The specification also describes human ROC2. ROC1 and ROC2 are similar to APC11, a subunit of the APC complex. The proteins stimulate cullin dependent ubiquitin ligase activity. ROC1 functions in vivo as an essential regulator of CDK inhibitor Sic1 degradation by the SCF (undefined) pathway. ROC proteins are useful for screening bioactive agents that interfere with the binding of ROC proteins with cullin proteins. Pharmaceutical formulations comprising ROC proteins are useful
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
                                                                                                                                                                                                                                 for diagnostic and therapeutic purposes, preferably for diagnosing and
                                                                                                                                                                                                                                                                                                                                                                                                                                                 ArgPheGluValLysLysTrpAsnAlaValAlaLeuTrpAlaTrpAspIleValValAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AsnCysAlaIleCysArgAsnHisIleMetAspLeuCysIleGluCysGlnAlaAsnGln
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AlaSerAlaThrSerGluGluCysThrValAlaTrpGlyValCysAsnHisAlaPheHis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181 GCGTCCGCTACTTCAGAAGAGTGTACTGTCGCATGGGGAGTCTGTAACCATGCTTTTCAC
                                                                                                                                                                                                                                                                                                                                                                                            MetAlaAlaAlaMetAspValAspThrProSerGlyThrAsnSerGlyAlaGlyLysLys
                                                                                                                                                                                                                                                                                                                                                                                                                Argececcagecarecageararececeagececaecaaeaacagecececececaaaaa
                                                                                 Novel nucleic acid encoding cullin regulating ring finger proteins, termed as ROC proteins similar to anaphase-promoting complex 11, for
                                                                                                                                                                                                                                                                Sequence 327 BP; 85 A; 75 C; 94 G; 73 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                               327
108
0
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0
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                       US-09-541-462B-2 (1-108) x AAA96882 (1-327)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TrpGluPheGlnLysTyrGlyHis 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gene therapy; chromosome mapping; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      therapeutic and diagnostic use.
                                                                                                                           Claim 1; Fig 2A; 83pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAC03896 standard; cDNA; 482
                                                                                                                                                                                                                                                                                               2.14e-66
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100.00%
           (UYNC-) UNIV NORTH CAROLINA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                   WPI; 2000-647235/62
                                                                                                                                                                                                                                                                                                                             Best Local Similarity:
Query Match:
                              Xiong Y, Ohta T;
                                                               P-PSDB; AAB19160
                                                                                                                                                                                                                                              treating tumours
                                                                                                                                                                                                                                                                                                                    Percent Similarity:
                                                                                                                                                                                                                                                                                     Alignment Scores:
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The present sequence is one of a large number of 5' ESTS derived from mRNAs encoding secreted proteins. An ORF has been identified within the sequence. The 5' ESTS were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. Ests sequences usually correspond mainly to the 3' untranalated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer cDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs and genomic DNAs. 5' ESTs are also used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design expression and secretion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           148
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      89 CGCTTTGAAGTGAAAAAGTGGAATAGCCGCTCTGGGCCTGGGGATATTGTGGTTGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21 ArgPheGluValLysLysTrpAsnAlaValAlaLeuTrpAlaTrpAspIleValValAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  41 AsnCysAlaIleCysArgAsnHisIleMetAspLeuCysIleGluCysGlnAlaAsnGln
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      149 AACTGTGCCATCTGCAGGAACCACATTATGGATCTTTGCATAGAATGTCAAGCTAACCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 AlaSerAlaThrSerGluGluCysThrValAlaTrpGlyValCysAsnHisAlaPheHis
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                                                                                                                                                                                                                                                                                                                                                                                                                      diagnostic, forensic, gene therapy and chromosome mapping procedures
                                                                                                                                                                                                                                                                                                                                                                                      5'ESTs and for
                                                                                                                                                                                                                                                                                                                                                            New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 482 BP; 116 A; 103 C; 121 G; 140 T; 0 U; 2 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; SEQ ID NO 3894; 71pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length:
Matches:
Conservative:
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                                                                                                                                                                                                                         Duclert A,
                                                       21-FEB-2000; 2000EP-00200610.
                                                                                                              99US-0122487P.
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                           P-PSDB; AAG03890
                                                                                                                                                                  (GEST ) GENSET
                                                                                                              26-FEB-1999;
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06-SEP-2000.
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DNA encoding a murine cullin-interacting RING-H2 finger protein (Rbx1).
                                                                                                                                                                                                                                                                                                                                                                              Cullin interacting RING-H2 finger protein, a component of von Hippel-Lindau tumor suppressor complex and Skpl-Cdc53p-F-box protein (SCF) ubiquitin ligase, useful for diagnosing and treating Ring box protein
                                                                                                                                             tumour suppressor; carcinoma; Ring box associated carcinoma; von Hippel-Lindau complex; ubiquitin conjugation; renal carcinoma; cerebellar hemangioblastoma; hemangioma; retinal angiomata;
                                                                                                                                Cullin-interacting RING-H2 finger protein; Ring box protein; Rbx1;
TGGGAATTCCAAAGTATGGGCAC 352
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                                                                                                                                                                                                                                                                                                              (OKLA-) OKLAHOMA MEDICAL RES FOUND.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 35; 37pp; English.
                                                                                                                                                                                                                                                                                                                                      Kamura
                                                                                                                                                                                                                                                                    25-FEB-2000; 2000WO-US004838.
                                                                                                                                                                                                                                                                                        99US-0121787P
                                         AAA74980 standard; DNA; 504
                                                                                      02-JAN-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                    Conaway RC,
                                                                                                                                                                             pheochromocytomas; ss
                                                                                                                                                                                                                                                                                                                                                                                                                 associated carcinomas
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                                                                                                                                                                                                                        WO200050445-A1.
                                                                                                                                                                                                                                                                                          26-FEB-1999;
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                                                                                                                                                                                                                                                                                                                                      Conaway JA,
                                                                AAA74980;
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The present sequence encodes a murine cullin-interacting RING-H2 finger protein (Ring box protein), designated Rbx1. The human Rbx1 polypeptide is a tumour suppressor. Human Rbx1 is useful for diagnosing a predisposition of a patient to certain carcinomas. It is also useful for treating Ring box protein associated carcinomas or augmenting explainted system in animals. Human Rbx1 is also useful for evaluating the effectiveness of a therapeutic treatment for Ring box associated carcinomas. Human Rbx1 can be used to screen for agents which augment or inhibit the activity of other cullin-containing ubiquitin ligase and of the VHL (von Hippel-Lindau) complex controlling the conjugation of ubiquitin or ubiquitinn-like proteins to various sets of target proteins. Carcinomas which may be treated include renal. carcinomas, cerebellar hemangioblastomas and hemangiomas, retinal angiomata and pheochromocytomas

Sequence 504 BP; 117 A; 107 C; 137 G; 143 T; 0 U; 0 Other;

	504	108	0	0	0	0
	Length:	Matches:	Conservative:	Mismatches:	Indels:	Gaps:
	3.86e-66	616.00	100.00%	100.00%	100.00\$	3
Alignment Scores:	Pred. No.:	Score:	Percent Similarity:	Best Local Similarity:	Query Match:	DB:

US-09-541-462B-2 (1-108) x AAA74980 (1-504)

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20		77
1 MetAlaAlaAlaMetAspValAspThrProSerGlyThrAsnSerGlyAlaGlyLysLys 20		18 ATGGCGGCGGCGATGGATGTGGATACCCCCAGCGGCACCAACAGCGGCGCGCGGGCAAGAAG 77
:AlaAlaAlaMetAspValA		3GCGGCGGCGATGGATGTGG
1 Mei	=	18 AT

21 ArgPheGluValLysLysTrpAsnAlaValAlaLeuTrpAlaTrpAspIleValValAsp 40

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The present invention describes an isolated tumour-associated antigenic target (TAT) nucleic acid comprising: (a) any of 4622 nucleotide sequences (see SEQ ID NO: 1 to 4622); (b) the full-length coding region of (a); (c) the complement of (a) or (b); (d) a sequence that has 80% sequence identity to (a)-(c); or (e) a sequence that hybridises to (a)-(c). Also described: (l) an expression vector comprising the above copression vector comprising the above comprising the above expression vector.

Comprising: (2) a host cell comprising the above expression vector; (3) a process for producing a polypeptide; (4) an isolated polypeptide

Comprising: (b) an amino acid sequence encoded by the full-
comprising the above polypeptide sequences; or (c) a sequence comprising the above polypeptide full sequences at 160% identical to (a) or (b); (5) a chimeric polypeptide

Comprising the above polypeptide fused to a heterologous polypeptide

an isolated antibody that binds to the above polypeptide; (7) a process for producing the above polypeptide; (9) a tumour-associated antigenic target (TAT)

C binding organic molecule that binds to the above polypeptide; (10) a composition of matter comprising the above (chimeric) polypeptide;
                                                                                                                                                                                                        PheHisCysIleSerArgTrpLeuLysThrArgGlnValCysProLeuAspAsnArgGlu 100
                                                                                                                                                                                                                         human; tumour-associated antigenic target; TAT; cytostatic; gene therapy; cancer; cell proliferative disorder; gene; ss.
                                                                                          .38 AACTGTGCCATCTGCAGGAACCACATTATGGATCTTTGTATCGAATGTCAGGCCAACCAG 197
                                                                                                                                                    GCGTCACTACTACCTACTATCCGAAGAGTGTACCATGCGGAGTCTGCAACCATGCTTTTCAT 257
                     CGCTTTGAAGTTAAAAAGTGGAATGCAGTGGCCCTCTGGGCCTGGGACATTGTGGTTGAT 137
                                                                                                                                80
                                                         9
                                                       AsnCysAlaIleCysArgAsnHisIleMetAspLeuCysIleGluCysGlnAlaAsnGln
                                                                                                                               AlaSerAlaThrSerGluGluCysThrValAlaTrpGlyValCysAsnHisAlaPheHis
Human tumour-associated antigenic target (TAT) cDNA sequence #4374.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New nucleic acid molecule and encoded polypeptide, for diagnosing, preventing or treating cell proliferative disorders such as cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; SEQ ID NO 4374; 5504pp; English.
                                                                                                                                                                                                                                                                                 101 TrpGluPheGlnLysTyrGlyHis 108
                                                                                                                                                                                                                                                                                                    318 TGGGAGTTCCAGAAGTATGGGCAT 341
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                                                                                                                                                                                                                                                                                                                                                                                             ADQ87496 standard; cDNA; 506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
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15-OCT-2003; 2003WO-US029126.

22-JUL-2004.

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with a carrier; (11) an article of manufacture comprising a container with a carrier; (11) an article of manufacture comprising a container and the composition of matter contained within the container; (12) methods of inhibiting the growth of a cell that expresses the above protein, where the growth of the cell is at least in part dependent upon a growth of the cell is at least in part dependent upon a growth of the cell is at least in part dependent upon a growth protein; (13) a method of determining the presence of a protein in a sample suspected of containing the presence of a protein in a sample suspected of containing the prosence of a tumour in a mammal; (16) a method for treating or preventing a cell proliferative disorder associated with increased expression or activity of the above protein; and (17) a method of binding an antibody, oligopeptide or cranic molecule to a cell that expresses the protein described above. The TAT sequences have cytostatic activities, and can be used in gene therapy. The composition and methods are useful for diagnosting, a medicament for the therapeutic treatment or diagnostic detection of a medicament for the therapeutic treatment or diagnostic detection of a cell proliferative disorder or cancer. The present sequence represents a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                human TAT cDNA sequence from the present invention.
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Sequence 506 BP; 126 A; 105 C; 124 G; 151 T; 0 U; 0 Other;

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CGCTTTGAAGTGAAAAAGTGGAATGCAGTAGCCCTCTGGGCCCTGGGATAFTGTGGTGGT 125
                                                                                                                                                                                                                                    AACTGTGCCATCTGCAGGAACCACATTATGGATCTTTGCATAGAATGTCAAGCTAACCAG 185
                                                                                                                                                                                                                                                                                   186 GCGTCCGCTACTTCAGAAGAGTGTACTGTCGCATGGGGAGTCTGTAACCATGCTTTTCAC 245
                                                                                                                                                                                                                                                             80
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                                                                                                                                                                  21 ArgPheGluValLysLysTrpAsnAlaValAlaLeuTrpAlaTrpAspIleValValAsp 40
                                                                                                                               AlaSerAlaThrSerGluGluCysThrValAlaTrpGlyValCysAsnHisAlaPheHis
                                                                                                                    1 MetAlaAlaAlaMetAspValAspThrProSerGlyThrAsnSerGlyAlaGlyLysLys
                                                                                                                                                                                                              41 AsnCysAlaIleCysArgAsnHisIleMetAspLeuCysIleGluCysGlnAlaAsnGln
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         Length:
Matches:
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Best Local Similarity:
Alignment Scores:
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ADQ87156 standard; cDNA; 506 BP (first entry) 07-OCT-2004 ADQ87156; RESULT 5 ADQ87156 BX8XXXXXXXXXXXXX

human; tumour-associated antigenic target; TAT; cytostatic; gene therapy; cancer; cell proliferative disorder; gene; ss. Human tumour-associated antigenic target (TAT) cDNA sequence #4032.

ното варіепв

WO2004060270-A2

1 MetalaalaalaaetaspvalaspThrProSerGlyThrAsnSerGlyAlaGlyLySLyS 20

US-09-541-462B-2 (1-108) x ADQ87156 (1-506)

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The present invention describes an isolated tumour-associated antigenic target (TAT) nucleic acid comprising: (a) any of 4622 nucleotide sequences (see SEQ ID Noil to 4622); (b) the full-length coding region of (a), (c) the complement of (a) or (b); (d) a sequence that has 80% esquences see SEQ ID Noil to 4622); (b) the full-length coding region of (a), (c) the complement of (a) or (b); (d) a sequence that has 80% esquence is esquence identity to (a) -(c); or (e) a sequence that hybridises to (a)-c); or (e) a sequence comprising the above expression vector; (3) conclision of comprising the above envised by 100 people of comprising; (a) an amino acid sequence encoded by any of the above nucleotide sequences of the above nucleotide sequence encoded by the full-comprising the above pulypeptide; (b) a chimeric polypeptide; (c) a comprising the above pulypeptide fused to a heterologous polypeptide; (d) an isolated oligopeptide; (f) a process of producing the antibody; (a) an isolated oligopeptide; (f) a process of comprising the above polypeptide; (g) a tumour-associated antispentide; (n) a comprising the above polypeptide; (g) a tumour-associated antispentide; (g) a tumour-associated antispentide; (g) a composition of matter comprising the above polypeptide; (g) a tumour-associated antispentide; (l) an article of manufacture comprising a container; of the composition of matter contained within the container; (l1) an article of manufacture comprising; (c) composition of matter contained within the container; (l2) methods of container; (l2) methods of described above; (l2) method of determining the process of a protein; (l3) a method of determining the presence of a protein; (l4) a method of determining the presence of a protein; (l4) a method of determining the above protein; (l4) a method of described above; (l5) methods of diagnosing the presence of a tumour in a sample suspecies on a clivity of the above of disorder associated with increased expresses the presence of a tumour and method of a cell that expresses t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              preventing or treating cancer. The composition is also used for preparing a medicament for the therapeutic treatment or diagnostic detection of a cell proliferative disorder or cancer. The present sequence represents a
                                                                                                                                                                                                                                                                                                                               New nucleic acid molecule and encoded polypeptide, for diagnosing, preventing or treating cell proliferative disorders such as cancer
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The present invention describes an isolated tumour-associated antigenic target (TAT) nucleic acid comprising: (a) any of 4622 nucleotide sequences (see SEQ ID NO:1 to 4622); (b) the full-length coding region of (a); (c) the complement of (a) or (b); (d) a sequence that has 80% (c). Also described: (1) an expression vector comprising the above nucleic acid; (3) a host cell comprising the above expression vector. (a) a process for producing a polypeptide; (4) an isolated polypeptide comprising; (a) an amino acid sequence encoded by the full-length coding region of the above nucleotide sequences; (b) an amino acid sequence encoded by the full-length coding region of the above nucleotide sequences; (c) a sequence (c) a sequence; (d) an amino acid sequence conded by the full-length coding region of the above nucleotide sequences; (c) a sequence; (d) an isolated or indicated action of the above polypeptide; (d) an isolated or isolated action of the above polypeptide; (f) an isolated or isolated that binds to the above polypeptide; (f) an isolated oligopeptide that binds to
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               human; tumour-associated antigenic target; TAT; cytostatic; gene therapy; cancer; cell proliferative disorder; gene; ss.
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66 CGCTTTGAAGTGAAAAGTGGAATGCAGTAGCCCTCTGGGCCTGGGGTATTGTGTGGTTGAT
                                                                                                                                                                           61 AlaSerAlaThrSerGluGluCysThrValAlaTrpGlyValCysAsnHisAlaPheHis
                                                                                                                                                                                                           186 GCGTCCGCTACTTCAGAAGAGTGTACTGTCGCATGGGGAGTCTGTAACCATGCTTTTCAC
                                                                                                        41 AsnCysAlaIleCysArgAsnHisIleMetAspLeuCysIleGluCysGlnAlaAsnGln
                                   21 ArgPheGluValLysLysTrpAsnAlaValAlaLeuTrpAlaTrpAspIleValValAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human tumour-associated antigenic target (TAT) cDNA sequence #1695.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New nucleic acid molecule and encoded polypeptide, for diagnosing, preventing or treating cell proliferative disorders such as cancer.
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the above polypeptide; (9) a tumour-associated antigenic target (TAT) binding organic molecule that binds to the above polypeptide; (10) a composition of matter comprising the above (chimeric) polypeptide, antibody, oligopeptide or TAT binding organic molecule, in combination with a carrier; (11) an article of manufacture comprising a container and the composition of matter contained within the container; (12) methods of inhibiting the growth of a cell that expresses the above protein, where the growth of the above protein; (13) a method of therapeutically treating a mammal having a cancerous tumour comprising cells that express the above protein; (14) a method of determining the presence of a protein in a sample suspected of containing the protein of a protein in a sample suspected of containing the protein of a method for treating or preventing a cell proliferative mammal; (16) a method for treating or preventing a cell proliferative of sprotein; and (17) a method of binding an antibody, oligopeptide or organic molecule to a cell that expressed the protein described above. The TAT sequences have cytostatic activities, and can be used in gene therapeuting or treating cancer. The composition and methods are useful for diagnosing, preventing or treating cancer. The composition is also used for preparing a method for the interapeut or treating care are useful for the tabove of a medicament for therapeut or treating care are useful to a cell that expresses the protein described by a method or treating cancer. The composition is also used for preparing a medicament for therapeut care are useful or a cell or the therapeut or treating care are useful to described and methods or treating care are useful for a cell or the therapeut or treating care are useful to a cell or the therapeut or treating care are useful to a cell or the therapeut or treating care are useful to a cell or the therapeut or treating care are useful to control or the control or care to the control or care to the control or care to the control or c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cell proliferative disorder or cancer. The present sequence represents a human TAT cDNA sequence from the present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence encodes a human cullin-interacting RING-H2 finger protein (Ring box protein), designated Rbx1. The polypeptide is a tumour suppressor. Rbx1 is useful for diagnosing a predisposition of a patient to certain carcinomas. It is also useful for treating Ring box protein associated carcinomas or augmenting metabolically deficient system in animals. Rbx1 is also useful for evaluating the effectiveness of a therapeutic treatment for Ring box associated carcinomas. Pbx1 can be used to screen for agents which augment or inhibit the activity of other cullin-containing ubiquitin ligase and of the VHL (von Hippel-Lindau) complex controlling the conjugation of ubiquitin or ubiquitin-like proteins to various sets of target proteins. Carcinomas which may be treated include renal carcinomas, cerebellar hemangioblastomas and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ArgPheGluValLysLysTrpAsnAlaValAlaLeuTrpAlaTrpAspIleValValAsp
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(Rbx1)"
cerebellar hemangioblastoma; hemangioma; retinal angiomata;
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                                                                                   Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 3; Page 35; 37pp; English.
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Best Local Similarity:
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                                                                                                                                                                                       WO200050445-A1
                                                                                                                                                                                                                                                                                           26-FEB-1999;
                                                   Homo sapiens
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The invention relates to human tumour-associated antigenic target (TAT) polypeptides, and their related nucleic acids. The TAT polypeptides are overexpressed in cancer tissues compared to normal tissues, and may thus server, as effective targets for the diagnosis and treatment of cancer in mammals. The invention also relates to nucleic acid and polypeptide equences at least 80% identical to the TAT nucleic acids and polypeptide; polypeptides, expression vectors and host cells comprising a TAT nucleic acid; an antibody specific for a TAT polypeptide; a peptide or organic molecule which binds to a TAT polypeptide; fusion proteins comprising a TAT polypeptide; and methods and compositions for the treatment or diagnosis of cancer in mammals. TAT polypeptides, nucleic acids, antibodies, antagonists, binding molecules and compositions are useful for diagnosing or treating a cell proliferative disorder associated with increased TAT expression, particularly cancers such as breast cancer, colorectal cancer, lung cancer, cancers such as breast cancer, colorectal cancer, und leukaemia. TAT nucleic acids may further be used as hybridisation probes, in chromosome acids may further be used as hybridisation probes, in chromosome acids may further be represents a TAT nucleic acids of the invention
                                      187 GCGTCCGCTACTTCAGAAGAGTGTACTGTCGCATGGGGAGTCTGTAACCATGCTTTTCAC 246
                                                                                                                                                                                                                                                                                                                                                                  Tumour-associated antigenic target (TAT) cDNA DNA326980, SEQ ID NO:6072.
                                                                                                                                                                                                                                                                                                                                                                                                         Tumour-associated antigenic target; TAT; human; overexpression; cancer; tumour; diagnosis; cell proliferative disorder; breast cancer; colorectal cancer; lung cancer; ovarian cancer; liver cancer; central nervous system cancer; bladder cancer; pancreatic cancer; cervical cancer; melanoma; leukaemia; hybridisation probe; chromosome identification; chromosome mapping; gene mapping;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New tumor-associated antigenic target polypeptides and nucleic acids, useful in preparing a medicament for treating or detecting a proliferative disorder, e.g. breast, lung, colorectal, ovarian or
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                                                                                                                    gene therapy; cytostatic; gene; ss.
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Conservative:
Mismatches:
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Sequence 508 BP; 126 A; 106 C; 124 G; 152
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STACHE-CRAIN B.
DICKSON M C.
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                                                                                                       Similarity:
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Pred. No.:
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The invention relates to an isolated polymucleotide comprising any one of 38043 cDNA sequences, appearing as ACH12789-ACH50831, whose sequence was determined by the technique of SBH (sequencing by hybridisation). Also included is a purified polypeptide comprising a sequence corresponding to a reading frame of the novel polymucleotide. The nucleic acid sequences corresponding to a reading frame of the novel polymucleotide. The nucleic acid sequence corresponding to a responsible expressed genes or for physical mapping of the human genome, in forensics, in assessing biodiversities, or in identifying mutations responsible for genetic disorders and other traits. The nucleotide corresponsible for genetic disorders and other traits. The nucleotide corresponsible for generating antisense DNA or RNA. The purified polypeptide protein, or in generating antisense DNA or RNA. The purified polypeptide is useful for generating antisense DNA/SET sequences. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from USPTO at sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          195 TGTGCCATCTGCAGGAACCACATTATGGATCTTTGCATAGAATGTCAAGCTAACCAGGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 AlaAlaAlaMetAspValAspThrProSerGlyThrAsnSerGlyAlaGlyLysElySArg
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Matches:
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SEQ ID NO 17191; 44pp; English.
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The invention relates to a novel isolated polynucleotide and the encoded polypeptide. The molecules of the invention demonstrate antinflammatory, neuroprotective, antianaemic, cyrostatic and vulnerary activities and may be useful in preparing a composition for diagnosing or treating inflammatory, haematopoietic, immune, neurodegenerative or stem cell disorders, such as aplastic anaemia or cancer, as well as for promoting wound healing. The molecules may also be utilised during gene therapy procedures. The current sequence is that of a human therapeutic DNA of the invention. The current sequence is not shown explicitly within the specification but can be accessed from the WIPO web-site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GCCATCTGCAGGAACCACATTATGGATCTTTGCATAGAATGTCAAGCTAACCAGGCGTCC 313
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                                                                                                                                                       Zhang J, Wehrman T, Wang Z, Ma Y_j Wang J, Ghosh M, Xue AJ, Weng G, Zhou P;
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                                                                                                                                                                                                                                                  New polynucleotide, useful in preparing a composition for diagnosing treating inflammatory, neurodegenerative or stem cell disorders, e.g. aplastic anemia or cancer for promoting wound healing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 3726 BP; 996 A; 955 C; 845 G; 930 T; 0 U; 0 Other;
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Matches:
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                                                                                                                                                                                                                                                                                                               Claim 1; SEQ ID NO 150; 718pp; English.
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ID ACN90161 standard; DNA; 4543 BP.
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                                                             30-SEP-2003; 2003WO-US030720
                                                                                          02-OCT-2002; 2002US-0416186P
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Chen R, Zhao QA,
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Best Local Similarity:
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WO2004080148-A2
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                                                                                                                                                        Tang YT,
                                                                                                                                                                       Wang D,
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The invention relates to an isolated polypeptide (I) associated with breast cancer which is encoded by a nucleic acid nolecule comprising a nucleotide sequence (SI). Further disclosed is an antibody that binds to the polypeptide of the invention. The activity of the polypeptide of the invention. The activity of the polypeptide of the invention as expostatic. The antibody is useful for detecting the presence of (I) in a sample. Nucleic acid molecules of the invention are useful in the detection of breast tumours. (I) is useful as a marker for breast cancer and in breast cancer therapy. Sequences given in records ACNV8851-ACN92934 represent nucleic acid markers associated with breast cancer. Note: The sequence listing doss not form part of the specification but may be obtained in electronic format from the USPTO web site at seqdata.uspto.gov/sequence.html?DocID=20030099974
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1025 GAAGTGAAAAAGTGGAATGCAGTAGCCCTCTGGGCCTGGGATATTGTGGTTGATAACTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        43 AlaIleCysArgAsnHisIleMetAspLeuCysIleGluCysGlnAlaAsnGlnAlaSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              63 AlaThrSerGluGluCysThrValAlaTrpGlyValCysAsnHisAlaPheHisPheHis
                                                                                                                                                                                                                                                                                                                                                                                   Novel isolated polypeptide associated with breast cancer, useful for detecting presence of polypeptide in sample, as a marker for breast
                                                                                          Cancer; breast; tumour; cytostatic; marker; detection; therapy; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 4543 BP; 1069 A; 1171 C; 1083 G; 1220 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length:
Matches:
Conservative:
Mismatches:
                                                            Breast cancer related marker, seq id 11311
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; SEQ ID NO 11311; 36pp; English
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                                                                                                                                                                                                                                                                                                                        Wang Y, Steinmann
                                                                                                                                                                                                                         18-JUL-2002; 2002US-00198846.
                                                                                                                                                                                                                                                        18-JUL-2001; 2001US-0306220P.
                                                                                                                                                                                                                                                                                          (MILL-) MILLENNIUM PHARM INC.
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607.00
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98.54%
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Best Local Similarity:
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                                                                                                                                                            US2003099974-A1.
                                                                                                                              Homo sapiens
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ACN90161;
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US-09-541-462B-2 (1-108) x ADQ92179 (1-503)
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Best Local Similarity:
Alignment Scores:
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TGCATCTCTCGCTGGCTCAAAACACGACAGGTGTGTCCATTGGACAACAGAGAGTGGGAA 786
                                                                                                                                                                                                                                                                                                                                                                                   New human DNA autoantigens, useful as assay, diagnostic, and prognostic reagents and for treating autoimmune disease, also related expression products and antibodies with similar uses.
                                                                                                                                              de; autoantigen; antibody; hybridoma; biosensor chip; extracorporeal differential diagnosis; autoimmune disease; tibsoomal protein; tubulin; dolichyl-diphospho-oligoscharide-glycosyl transferase; multiple sclerosis; theumatoid arthritis; epitope mapping; affinity chromatography; electrophoresis; autoantibody apheresis;
                                                                                                                               Human autoantigen DNA fragment MPMGp800L05536.
                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; SEQ ID NO 160; 110pp; German.
                PheGlnLysTyrGlyHis 108
                                                                        ADQ92179 standard; DNA; 503 BP
                                                                                                                                                                                                                                                                                  23-DEC-2002; 2002WO-EP014731
                                                                                                                                                                                                                                                                                                     23-DEC-2002; 2002WO-EP014731
                                   TTCCAAAGTATGGGCAC
                                                                                                            07-OCT-2004 (first entry)
                                                                                                                                                                                                         interference; RNAi
                                                                                                                                                                                                                                                                                                                                                 Thiesen H, Lorenz P;
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                                                                                                                                                                                                                                                                                                                       (THIE/) THIESEN H.
                                                                                                                                                                                                                                                                                                                                (LORE/) LORENZ P.
                                                                                                                                                                                                                                             WO2004058972-A1
                                                                                                                                                                                                                           Homo sapiens.
                                                                                                                                                                                                                                                                15-JUL-2004.
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ADQ92179
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4 AlaMetAspValAspThrProSerGlyThrAsnSerGlyAlaGlyLysLysBysArgPheGlu

503 105 0 0

Conservative: Mismatches: Length: Matches:

53e-64 603.00 100.00% 100.00% 97.89%

. No. :

Indels: Gaps: 3 GCGATGGGATGTGCGCTAGCGCGCACCAACAGCGGCGCGGGCAAGAAGCGCTTTGAA

24 VallysLysTrpAsnAlaValAlaLeuTrpAlaTrpAspIleValValAspAsnCysAla 63 GIGAAAAAGIGGAAIIGCAGIAGCCCICIGGGCCIGGAIAIIGIGGGIIGAIAACIGIGCC 182

44 IleCysArgAsnHisIleMetAspLeuCysIleGluCysGlnAlaAsnGlnAlaSerAla

83

63

104 GlnLysTyrGlyHis 108 CAAAAGTATGGGCAC 317

303

183 ACTTCAGAAGAGTGTACTGTCGCATGGGGAGTCTGTAACCATGCTTTTCACTTCCACTGC 242

64 ThrSerGluGluCysThrValAlaTrpGlyValCysAsnHisAlaPheHisPheHisCys

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DNA Sequences encoding 7-transmembrane G-protein coupled protein receptors characteristic of hematopoietic stem cells, useful for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention relates to murine coding sequences for 7-transmembrane G-protein coupled protein receptors (7TM-GPCRs). The present sequence is one such murine 7TM-GPCR coding sequence. The present
                                                                                                                                                                          Murine 7-transmembrane G-protein coupled receptor coding sequence #104.
                                                                                                                                                                                                                               Murine, hematopoietic stem cell; signalling, vaccine, 7TM-GPCR; 7-transmembrane G-protein coupled protein receptor; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pereira
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Page 62; 176pp; English
AAH97860 standard; DNA; 539 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14-FEB-2001; 2001WO-US004700.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14-FEB-2000; 2000US-0182377P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (IMCL-) IMCLONE SYSTEMS INC. (UYPR-) UNIV PRINCETON.
                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lemischka IR, Witte L,
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                                                                                                                                                                                                                                                                                                                                                                                   WO200160999-A1.
                                                                                                               10-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                              23-AUG-2001.
                                                       AAH97860;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      eukemia.
This invention describes novel human DNA autoantigens which are used to produce recombinant expression vectors; prokaryotic or eukaryotic cells; poly- or mono-clonal antibodies (Ab) specific; hybridomas that express monoclonal Ab; biosensor chips having an addressable sequence pattern as probes; medical or diagnostic instruments that include the biosensor; for extracorporeal differential diagnosis of autoimmune diseases and corteins; tubulins; dolichyl-diphospho-oligosaccharide-glycosyl proteins; tubulins; dolichyl-diphospho-oligosaccharide-glycosyl cransferases and proteins. The autoantigen may be labelled conventionally with radioisotopes, coloured or fluorescent groups, or a member of the biotin/avidin pair, or colloidal gold. The autoantigens can be directed against mitochondria, liver-kidney microsomes; histidyl-tRNA; nuclear membrane; neutrophilin/cytoplasm; insect cells; epidermal intracellular cor basal membrane antigens; Golg or cell nuclei, or associated with multiple sclerosis or rheumatoid arthritis. They are useful for epitope cor mapping; in affinity chromatography or electrophoresis; for diagnosis, prognosis, control of treatment or therapeutic response of autoimmune con diseases, particularly in vitro differential diagnosis of autoimmune con diseases; to produce biosensor chips or for autoantibody apheresis.

C Autoantigon DNA can be used for therapeutic RNA interference against autoantibodies. Biochips that carry the new materials are useful in management of autoantibodies. Biochips that carry the new materials are useful in management or medical and diagnostic instruments. ADQ92020-ADQ92280 represent human
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Seguence 503 BP; 131 A; 102 C; 120 G; 150 T; 0 U; 0 Other;

autoantigens.

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and its corresponding protein are useful in the present sequence treatment of diseases associated with inappropriate 7TM-GPCR expression. 7TM-GPCRs identify specific signalling molecules, to activate an effector esugnalling cascade that triggers an intracellular response and
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                                                                                                                                                                                                                                                                                                                                                       240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Murine 7-transmembrane G-protein coupled receptor coding sequence #106
                                                                                                                                                                                                                                                                       GTTAAAAAGTGGAATGCAGTGGCCCTCTGGCCCTGGGACATTGTGTGGTTGATAACTGTGCC
                                                                                                                                                                                                                                                                                                                                                  ThrSerGluGluCysThrValAlaTrpGlyValCysAsnHisAlaPheHisPheHisCys
                                                                                                                                                                                                           AlametAspValAspThrProSerGlyThrAsnSerGlyAlaGlyLysLysArgPheGlu
                                                                                                                                                                                                                     GCGATGGATGTGATTACCCCCAGCGGCACCAACAGCGGCGGCGGGCAAGAAGCGCTTTGAA
                                                                                                                                                                                                                                                  VallyslysTrpAsnAlaValAlaLeuTrpAlaTrpAspIleValValAspAsnCysAla
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                                                                                                                                                                                                                                                                                                       ATCTGCAGGAACCACATTATGGATCTTTGTATCGAATGTCAGGCCAACCAGGCGTCAGCT
                                                                                  Other;
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Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                standard;
                                                                                                                                   Percent Similarity:
Best Local Similarity:
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                                                                                  Sequence 539
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                                                                                                      Alignment Scores:
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DNA Sequences encoding 7-transmembrane G-protein coupled protein receptors characteristic of hematopoietic stem cells, useful for treating leukemia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     84 IleSerArgTrpLeuLysThrArgGlnValCysProLeuAspAsnArgGluTrpGluPhe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AlametAspValAspThrProSerGlyThrAsnSerGlyAlaGlyLysLysLygArgPheGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             44 IleCysArgAsnHisIleMetAspLeuCysIleGluCysGlnAlaAsnGlnAlaSerAla
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EST associated with lactation/muscle/fat deposition #4677
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 586 BP; 140 A; 122 C; 164 G; 159 T; 0 U; 1 Other;
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Warren WC;

Tao N,

New nucleic acid associated with lactation, and muscle and fat deposition, useful for genome mapping, gene identification and analysis, cattle breeding, or for genetically improving cattle.

Claim 2; SEQ ID NO 4677; 245pp; English.

The invention relates to a purified nucleic acid molecule associated with lactation or muscle and fat deposition (designated IMPD), derived from cattle, and the LMFD nucleic acid can specifically hybridise to a second nucleic acid molecule comprising any of 1512 nuclectide sequences, appearing as ABX34336-ABX49947, or complements of them. Also included are cid in a transformed call having a nucleic acid comprising an IMPD nucleic acid linked to a promoter and a 3 non-translated sequence that functions in the cell to cause termination of transcription and addition of polyadenylated ribonucleotides to a 3' end of the mRNA molecule; and (2) determining a level or pattern of a molecule in a bovine cell or tissue comprising: (a) incubating a marker nucleic acid (comprising any of the 1512 nucleic acid molecule obtained from the bovine cell or tissue, where hybridisation between the marker nucleic acid and the complementary nucleic acid molecule obtained from the bovine cell or tissue, where hybridisation between the marker nucleic acid and the detection of the complementary nucleic acid permits the detection of the molecule. The LMFD nucleic acid is used for the detecting the level or pattern of the molecule. The LMFD nucleic acid is used for determining a level or pattern of a molecule in a bovine cell or tissue. It is useful for genome mapping, gene identification and analysis, cattle for genetically improving cattle. The present sequence is one of the 1512 bovine LMFD SST (expressed sequence tag) nucleic acids. Note: The present sequence was not shown in the specification but was obtained in electronic format from the USPTO web site: sequence. Seqdata uspto gov/sequence.

Sequence 380 BP; 98 A; 87 C; 103 G; 92 T; 0 U; 0 Other;

Alignment Scores:
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 Percent Similarity:
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Search completed: June 24, 2005, 09:01:45 Job time : 449 secs

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Description	-242-535A-43377 Sequence 4337 -085-783A-43377 Sequence 4337	-10-242-535A-35025 Sequence 35025, -10-085-783A-35025 Sequence 35025,	-10-242-535A-39933 Sequence 39933,	-10-085-783A-39933 Sequence 39933, -10-242-535A-57254 Sequence 57254,	-10-085-783A-57254 Sequence 57254,	-10-242-535A-56068 Sequence 56068, -10-085-7832-56068 Semience 56068.	-10-913-937-5 Sequence 5, Appl	-10-913-937-3 Sequence 3, Appl	-10-242-535A-46292 sequence 46292, -10-085-783A-46292 Sequence 46292,	-09-918-995-17191 Sequence 17191,	-10-198-846-11311 Sequence 11311, -10-242-535A-54751 Sequence 54751,	-10-085-783A-54751 Sequence 54751,	79-360-352-46// -10-357-930-25604 Seguence 2560	-10-240-965-99 Sequence 99,	-10-723-860-1383 Sequence 1383	-10-203-823-302 -10-723-860-5852 Sequence 5852	-10-242-535A-47656 Sequence 4765	-10-085-783A-47656 Sequence 4765 -10-767-701-12172 Sequence 1217	-10-487-901-4266 Sequence 42	-10-487-901-4271 Sequence 4271 -10-487-901-4270 Sequence 4270	-10-487-901-4265 Sequence 4265	-10-487-901-4263 Sequence 4263	-10-43/-963-11395 Sequence 1133 -10-425-114-25647 Semience 2564	-10-487-901-4261 Sequence 4261	-10-487-901-4262 Sequence 4262	-10-021-323-10545 sequence 1054 -10-767-795-687 Semience 687.	-10-424-599-6074 Sequence 6074	19-770-791-20 Sequence 20, A	-10-425-115-10631 Sequence 19631, -10-767-795-688 Sequence 688, A	-10-487-901-4264 Sequence 4264,	-10-767-701-12171 S -10-242-535A-52747 S	ALIGNMENTS	0242535A	s and Meth 10/242,535	s and Methods Relatiing to Osteoarthriti 10/242,535A 2 885,783
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Sequence 43377, Application No. US20040037841A1

GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Chondrodene Inc.

TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis

FILE REFERENCE: 4231/2002

CURRENT APPLICATION NUMBER: US/10/085,783A

CURRENT FILING DATE: 2002-02-28

PRIOR APPLICATION NUMBER: US 60/305,340

PRIOR PILING DATE: 2001-07-13

PRIOR PILING DATE: 2001-03-12

PRIOR PILING DATE: 2001-03-12

PRIOR FILING DATE: 2001-03-12

PRIOR FILING DATE: 2001-03-28

NUMBER OF SEQ ID NOS: 58994

SOFTWARE: PatentIn version 3.2

LENGTH: 433
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Conservative:
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PRIOR FILING DATE: 2001-03-12
PRIOR APPLICATION NUMBER: US 60/271,955
PRIOR FILING DATE: 2001-02-28
NUMBER OF SEQ ID NOS: 58994
SOFTWARE: Patentin version 3.2
SEQ ID NO 43377
LENGTH: 433
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US-10-242-535A-43377
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publication No. US20040013663A1

general information No. US20040013663A1

general information No. US20040013663A1

APPLICANT: ChondroGene Inc.

APPLICANT: ChondroGene Inc.

TITLE OF INVENTY DATE:

CURRENT APPLICATION NUMBER: US/10/242,535A

CURRENT FILING DATE: 2002-09-12

PRIOR APPLICATION NUMBER: US 60/305,340

PRIOR FILING DATE: 2001-07-13

PRIOR FILING DATE: 2001-07-13

PRIOR FILING DATE: 2001-03-12

PRIOR FILING DATE: 2001-03-28

SOFTWARE: Patentin version 3.2

SEQ ID NO 35025

LENGTH: 453
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US-10-242-535A-39933

Sequence 39933, Application US/10242535A

Publication No. US20040013663A1

GENERAL INFORMATION:

APPLICANT: ChondroGene Inc.

APPLICANT: ChondroGene Inc.

APPLICANT: Compositions and Methods Relating to Osteoarthritis

FILE REFERENCE: 4231/2005

CURRENT APPLICATION NUMBER: US/10/242,535A

CURRENT APPLICATION NUMBER: US 60/205,783

PRIOR PILING DATE: 2002-09-12

PRIOR FILING DATE: 2001-07-13

PRIOR FILING DATE: 2001-07-13

PRIOR FILING DATE: 2001-07-13

PRIOR FILING DATE: 2001-07-13

PRIOR FILING DATE: 2001-02-28

NUMBER OF SEQ ID NOS: 58994

SOFTWARE: PatentIn version 3.2

SEQ ID NO 39933

LENGTH; 467
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                             Sequence 39933, Application US/10085783A; Publication No. US20040037841A1; GENERAL INFORMATION:
APPLICANT: ChondroGene Inc.
APPLICANT: Liew, C.C.
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ORGANISM: Human
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Pred. No.:
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GENERAL INPORMATION:
TIPLE OF INVERTION: C.C.
TITLE OF INVERTION: Compositions and Methods Relatiing to Osteoarthritis FILE REFERENCE: 4231/2002; CURRENT APPLICATION NUMBER: US/10/085,783A; CURRENT PILING DATE: 2002-02-28; FILOR PAPLICATION NUMBER: US 60/305,340; FRIOR PILING DATE: 2001-07-13; FRIOR PILING DATE: 2001-07-13; FRIOR APPLICATION NUMBER: US 60/275,017; FRIOR APPLICATION NUMBER: US 60/275,017; FRIOR APPLICATION NUMBER: US 60/271,955; FRIOR PILING DATE: 2001-02-28; NUMBER OF SEQ ID NOS: 58994; SOFTWARE: PAECHLIN Version 3.2; SEQ ID NO 35025; LENGTH 453; FRIOR ELLING DATE: 2001-02-28; ELENGTH: 453; FRIOR ELLING DATE: 2001-03-12; ELENGTH: 453; FRIOR ELLING DATE: 453; FRI
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US-10-085-783A-35025
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US-10-085-783A-35025
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CURRENT PAPLICATION NUMBER: US/10/085,783A
CURRENT PILING DATE: 2002-02-8
PRIOR APPLICATION NUMBER: US 60/305,340
PRIOR PELING DATE: 2001-07-13
PRIOR PELING DATE: 2001-07-13
PRIOR PELING DATE: 2001-03-12
PRIOR FILING DATE: 2001-03-12
PRIOR FILING DATE: 2001-03-12
PRIOR FILING DATE: 2001-03-28
NUMBER OF SEQ ID NOS: 58994
SOFTWARE: Patentin Version 3.2
LENGTH: 467
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US-10-242-535A-57254
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                                                                                                                             TYPE: DNA
ORGANISM: Human
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Pred. No.:
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US-10-085-783A-57254

US-10-085-783A-57254

US-10-085-783A-710N

US-10-085-783A

US-10-085-783A

UNRENT COMPOSITIONS and Methods Relatiing to Osteoarthritis

FILE REFERENCE: 4231/2002

UURRENT FILING DATE: 2002-02-28

PRIOR PPLICATION NUMBER: US 60/205,017

PRIOR PPLICATION NUMBER: US 60/275,017

PRIOR PLING DATE: 2001-07-13

PRIOR PLING DATE: 2001-07-13

PRIOR PLING DATE: 2001-02-28

NUMBER OF SQ ID NOS: 58994

SOFTWARE: PatentIn version 3.2

SEQ ID NO 57254

LENGTH: 471

LENGTH: 471
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Best Local Similarity:
Query Match:
DB:
; TYPE: DNA
; OKGANISM: Human
US-10-242-535A-57254
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81 PheHisCysIleSerArgTrpLeuLysThrArgGlnValCysProLeuAspAsnArgGlu 100
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Matches:
Conservative:
Mismatches:
Indels:
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TITLE OF INVENTION: Compositions and Methods Rel.
FILE REFERENCE: 4231/2002
CURRENT APPLICATION NUMBER: US/10/085,783A
CURRENT FILING DATE: 2002-02-28
FRIOR PELICATION NUMBER: US 60/305,340
FRIOR FILING DATE: 2001-07.13
FRIOR FILING DATE: 2001-03-12
FRIOR PELING DATE: 2001-03-12
FRIOR PELING DATE: 2001-03-12
FRIOR FILING DATE: 2001-03-13
FRIOR FILING DATE: 2001-03-14
FRIOR FILING DATE: 2001-03-15
FRIOR FILING DATE: 2001-03-15
FRIOR FILING DATE: 2001-03-16
FRIOR FILING DATE: 2001-03-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           78-10-085-783A-56068
; Sequence 56068, Application US/10085783A
; Publication No. US20040037841A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
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NAME/KEY: misc feature

CCATION: (437)...(437)

OTHER INFORMATION: n is a, c, g,

FEATURE:

NAME/KEY: misc feature

LOCATION: (455)...(455)

COTHER INFORMATION: n is a, c, g,

US-10-085-783A-56068
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Best Local Similarity:
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ORGANISM: Human
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APPLICANT: Liew, C.C.
TITLE OF INVENTION: Compositions and Methods Relatiing to Osteoarthritis
FILE REFERENCE: 4221/2005
CURRENT APPLICATION NUMBER: US/10/242,535A
CURRENT PILING DATE: 2002-09-12
FRIOR APPLICATION NUMBER: US 60/305,783
PRIOR FILING DATE: 2002-02-28
FRIOR PELING DATE: 2001-07-13
PRIOR FILING DATE: 2001-03-12
PRIOR PILING DATE: 2001-03-12
PRIOR APPLICATION NUMBER: US 60/275,017
PRIOR APPLICATION NUMBER: US 60/275,017
PRIOR APPLICATION NUMBER: US 60/275,017
PRIOR APPLICATION NUMBER: US 60/271,955
PRIOR APPLICATION NUMBER: US 60/271,955
PRIOR APPLICATION NUMBER: OS 6001-03-28
NUMBER OF SEQ ID NOS: 58994
SOFTWARE: Patentin version 3.2
LENGTH: 472
                                                                                                                                                                    77 CGCTTTGAAGTGAAAAAGTGGAATGCAGTAGCCCTCTGGGCCTGGGATATTGTGGTTGAT 136
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  US-09-541-462B-2 (1-108) x US-10-085-783A-57254 (1-471)
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Matches:
Conservative:
Mismatches:
Indels:
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) LOCATION: (455)..(455)
) OTHER INFORMATION: n is
US-10-242-535A-56068
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LOCATION: (437)...(437)
OTHER INFORMATION: n is
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Publication No. US20050019813A1

GENURCAL INFORMATION:

APPLICANT: Conaway, Joan A.

APPLICANT: Conaway, Ronald C.

APPLICANT: Oklamoma Medical Research Foundation

ITITLE OF INVENTION: Complex and SCF Ubiquitin Ligase

FILE REFERENCE: 02004-004-0046000US

CURRENT APPLICATION NUMBER: US/09/914,324

FRIOR FILING DATE: 2001-08-22

FRIOR FILING DATE: 1999-02-25

FRIOR FILING DATE: 1999-02-25

FRIOR FILING DATE: 2000-02-25

FRIOR F
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PheHisCys1leSerArgTrpLeuLysThrArgGlnValCysProLeuAspAsnArgGlu 100
                                 258 TTCCACTGCATCTCTCGATGGCTCAAAACGAGGCAGGTGTGTCCCTTGGACAACAGAGA 317
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CTHER INFORMATION: Rbx1
US-10-913-937-3
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ORGANISM: Homo sapiens
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Best Local Similarity:
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sequence 5, Application US/10913937

sequence 5, Application No. US20050019813A1

sequence 5, Application No. US20050019813A1

sequence 5, Application No. US20050019813A1

septicant: Conaway, Joan A.

septicant: Conaway, Ronald C.

APPLICANT: Conaway, Ronald C.

APPLICANT: Conaway, Ronald C.

TITLE OF INVENTION: Novel Component of von Hippel-Lindau Tumor Suppressor

TITLE OF INVENTION: Complex and SCF Ubiquitin Ligase

TITLE OF INVENTION: Complex and SCF Ubiquitin Ligase

TITLE OF INVENTION: Complex and SCF Ubiquitin Ligase

CURRENT APPLICATION NUMBER: US/10/913,937

CURRENT FILING DATE: 2004-08-05

PRIOR APPLICATION NUMBER: US 60/121,787

PRIOR APPLICATION NUMBER: WO FCT/US00/0483B

PRIOR FILING DATE: 1099-02-25

NUMBER OF SEQ ID NOS: 12

SOFTWARE: PatentIN Ver. 2.1

SEQ ID NO 5

LENGTHARE: PatentIN Ver. 2.1
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    140 AACTGTGCCATCTGCAGGAACCACATTATGGATCTTTGCATAGAATGTCAAGCTAACCAG 199
                                                                                              200 GCGTCCGCTACTTCAGAAGAGTGTACTGTCGCATGGGGAGTCTGTAACCATGCTTTTCAC 259
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                                                                      61 AlaSerAlaThrSerGluGluCysThrValAlaTrpGlyValCysAsnHisAlaPheHis
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; OTHER INFORMATION: Rbx1
US-10-913-937-5
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Query Match:
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ORGANISM: Mus sp.
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Pred. No.:
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                                                                    US-10-242-535A-46292

Sequence 46292, Application US/10242535A

PUDICARIAL INFORMATION:
APPLICANT: ChondroGene Inc.
APPLICANT: ChondroGene Inc.
APPLICANT: ChondroGene Inc.
TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
FILE REFERENCE: 4231/2005
CURRENT APPLICATION NUMBER: US/10/242,535A
CURRENT PILING DATE: 2002-09-12
FRIOR APPLICATION NUMBER: US 60/305,340
FRIOR FILING DATE: 2002-07-13
FRIOR PILING DATE: 2001-07-13
FRIOR PILING DATE: 2001-07-13
FRIOR PILING DATE: 2001-07-13
FRIOR APPLICATION NUMBER: US 60/275,017
FRIOR FILING DATE: 2001-03-12
FRIOR FILING DATE: 2001-03-13
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Sequence 46292, Application US/10085783A

GENERAL INFORMATION:

APPLICANT: ChondroGene Inc.

APPLICANT: Liew, C.C.

TITLE OF INVENTION: Compositions and Methods Relatiing to Osteoarthritis
FILE REFERENCE: 4231/2002

CURRENT APPLICATION NUMBER: US/10/085,783A
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TGGGAATTCCAAAAGTATGGGCAC 330
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US-10-242-535A-46292
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US-10-085-783A-46292
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TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES
TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
FILE REFERENCE: 20411-756
CURRENT PAPLICATION NUMBER: US/09/918,995
CURRENT FILING DATE: 2001-07-30
PRIOR FILING DATE: 1999-01-20
NUMBER OF SEQ ID NOS: 38054
SOFTWARE: FRACESEQ FOR Windows Version 3.0
SEQ ID NO 17191
LENGTH: 476
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Matches:
Conservative:
Mismatches:
CUKKENT FILING DATE: 2002-02-28

PRIOR APPLICATION NUMBER: US 60/305,340

PRIOR FILING DATE: 2001-07-13

PRIOR APPLICATION NUMBER: US 60/275,017

PRIOR FILING DATE: 2001-03-12

PRIOR FILING DATE: 2001-03-12

PRIOR FILING DATE: 2001-02-28

NUMBER OF SEQ ID NOS: 58994

SOFTWARE: PALENTIN VERSION 3.2

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LENGTH: 523
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; OTHER INFORMATION: n = A,T,C ous-09-918-995-17191
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Percent Similarity:
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Query Match:
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                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Human
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US-09-918-995-17191
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Eukaryota, Merazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Merazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 354)

Su (bazaki, Y.; Furuno, M.; Kasukawa, T.; Adachi, J.; Bono, H.; Kondo, S.; Nikaido, I.; Osato, N.; Saito, R.; Suzuki, H.; Yamanaka, I.; Kiyosawa, H.; Yagi, K.; Tomaru, Y.; Hasegawa, Y.; Nogami, A.; Schonbach, C.; Gojobori, T.; Baldarelli, R.; Hill, D. P.; Bult, C.; Hume, D. A.; Quackenbush, J.; Schrimi, L. M.; Kanapin, A.; Matsuda, H.; Batalov, S.; Beisel, K.W.; Blake, J. A.; Bradt, D.; Brusic, V.; Chothia, C.; Corbani, L.E.; Coussins, S.; Dalla, E.; Dragani, T. A.; Fletcher, C.F.; Forrest, A.; Frazer, K.S.; Gasterland, T.; Gariboldi, M.; Gissi, C.; Godzik, A.; Gough, J.; Grimmond, S.; Gustincich, S.; Hirokawa, N.; Jackson, I.J.; Jarvis, R.M.; King, B. L.; Konagaya, A.; Kirochkin, I. V.; Lee, Y.; Lenhard, B.; Lyons, P.A.; Maglott, D.R.; Numata, K.; Okido, T.; Perrest, R.M.; King, B. L.; Konagaya, Ravasi, T.; Reed, J. C.; Reed, D. J.; Reid, J.; Ring, B. Z.; Ringwald, M.; Sandelin, A.; Schneider, C.; Semple, C.A.; Setou, M.; Shimada, K.; Sultana, R.; Takenaka, Y.; Taylor, M.S.; Tesadale, R.D.; Tomita, M.; Verardo, R.; Walming, L.G.; Wang, Y.; Yanagisawa, M.; Yang, I.;
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BF956282
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-MODEL=frame+ p2n.model-DEV=x1h
-Q=/Cgn2_1/USPTO_expool/US09541462/runat_23062005_122624_9491/app_query.fasta_1.263
-Q=/Cgn2_1/USPTO_expool/US09541462/runat_23062005_122624_9491/app_query.fasta_1.263
-Q=/Cgn2_1/USPTO_expool/US09541462/runat_23062005_1-LGODEXT=0
-UNTIS=b1te -START=1 -END=-1 -MATRIX=b10sum62 -TRANS=human40.cdi -LIST=45
-UNTIS=b1te -START=1 -END=-1 -MATRIX=b10sum62 -TRANS=human40.cdi -LIST=45
-UNTIS=btc -OFFR=2 - MATRIX=B100 - TRE_NIN=0 - ALIGN=15 - MODE=LOCAL
-UTREPT=ptc -NORM=ext -HEAPSIZE=560 - MINLEN=0 -MAXLEN=200000000.
-USER=US09541462_@CGN 1 1 3437_@runat_23062005_122624_9491 -NCPU=6 -ICPU=3
-NO MAAP -LARGEQUERY -NGG SCORES=0 - WAIT -DSPELOCK=100 -LONGLOG
-DBV TIMEOUT=120 -WARN TIMEOUT=30 -THEADS=1 -KGAPOP=10 -KGAPORT=0.5 -FGAPOP=6
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                               GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                       - nucleic search, using frame_plus_p2n model
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUMMARIES
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Maximum Match 100%
Listing first 45 summaries
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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Maximum DB seq length: 200000000
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gb_est4::*
gb_est5::*
gb_est6::*
gb_gss1::*
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Database :

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Result No.

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MEDLINE PUBMED JOURNAL

COMMENT

TITLE

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Bukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus. E. (bases 1 to 358)
S. Akimura, T., Arakawa, T., Carninci, P., Furuno, M., Hanagaki, T., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Imotani, K., Ishi, Y., Ito, M., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Matsuyama, T., Nakamura, M., Nomi, K., Nomura, K., Numasaki, R., Okada, T., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T., Tanaku, M., Tagawa, A., Takahashi, F., Takaku, Akahira, S., Muramatsu, M. and Hayashizaki, Y., Watahiki, A., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BB871840 RIKEN full-length enriched, 13 days embryo spinal cord Mus musculus cDNA clone G630032107 5', mRNA sequence.
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Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Yoshihide Hayashizaki
Laboratory for denome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
T-7.22 Suchiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-922
Pax: 81-45-503-9216
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Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. . 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T.,
and Hayashizaki,Y.
75 CGCTTTGAAGTTAAAAAGTGGAATGCAGTGGCCCTCTGGGCCTGGGACATTGTGGTTGAT 134
                                                                                                                                                                                                                                                                                                                                                        81 PheHisCysIleSerArgTrpLeuLysThrArgGlnValCysProLeuAspAsnArgGlu 100
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                                                                                                                                                                                                                              61 AlaSerAlaThrSerGluGluCysThrValAlaTrpGlyValCysAsnHisAlaPheHis 80
                                                                                                                                                                                                                                                                  41 AsnCysAlaIleCysArgAsnHisIleMetAspLeuCysIleGluCysGlnAlaAsnGln
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Raizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S.,
Hirozanie,T., Indiani,K., Ishii,Y., Itoh,M., Kawai,J., Konno,H.,
Miyazaki,A., Murata,M., Nakamura,M., Nomura,K., Numazaki,R.,
Ohno,M., Sakai,K., Sakazume,N., Sasaki,D., Sato,K., Shibata,K.,
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Computational Analysis of Full-Length Mouse cDNAs Compared with
Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
Genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer. Genome Res.
10 (11), 1757-177 (2000)
Computer-based methods for the mouse full-length cDNA
encyclopedia: real-time sequence clustering for construction of a
nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
cDNA library was prepared and sequence din Nouse Ganome
Encyclopedia Project of Genome Exploration Research Group in Riken
prepare monse fishers
   Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P., Hayatsu, N., Hirozane-Kishikawa, T., Konno, H., Nakamura, M., Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K., Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K., Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, B.S., Rogers, J., Birney, E. and Hayashizaki, Y.
Analysis of the mouse transcriptome based on functional annotation Nature 420, 563-573 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                 Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9226
Fax: 81-45-503-9216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            prepare mouse tissues.
Tissues were provided by Vassilis Aidinis ( Biomedical Sciences
Research Center 'Al. Fleming' Institute of Immunology 14-16 Al.
Fleming street 16672 Vari, Greece ) whose assistance we gratefully
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/db_xref="taxon:10090"
/clone="L730004M21"
/tissue_type="whole joints"
/clone_lib="RIKEN full-length enriched, whole joints"
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Location/Qualifiers

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FEATURES

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21 ArgPheGluValLysLysTrpAsnAlaValAlaLeuTrpAlaTrpAspIleValValAsp 40

Query Match: DB:

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S. Mazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Nikaido, I., Osato, N., Saito, R., Suzuki, H., Yamanaka, I., Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Kuyonach, C., Gojobori, T., Schriml, L. M., Kanapin, A., Matsuda, H., Batalov, S., Beisel, K.W., Elake, J.A., Bradt, D., Brusic, V., Chothia, C., Corbani, L. B., Cousins, S., Dalla, B., Dragani, T. A., Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Girimnond, S., Gustincich, S., Hirokawa, N., Jackson, I.J., Jarvis, B.D., Kanaja, A., Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Maglott, D.R., Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T., Numata, K., Okido, T., Pavan, W.J., Pertea, G., Pescole, G.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BY035215
358 bp mRNA linear EST 06-DEC-2002
8035215 RIKEN full-length enriched, 11 days pregnant adult female
placenta Mus musculus cDNA clone I530017M08 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 AlaSerAlaThrSerGluGluCygThrValAlaTrpGlyValCygAsnHisAlaPheHis
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/strain="C57BL/6J"
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Petrovsky, N., Pillai, R., Pontius, J.U., Qi, D., Ramachandran, S., Ravasi, T., Reed, J.C., Reed, D.J., Reid, J., Ring, B.Z., Ringwald, M., Sandelin, A., Schneider, C., Semple, C.A., Setou, M., Shimada, K., Sultana, R., Takenaka, Y., Taylor, M.S., Teasdale, R.D., Tomita, M., Verardo, R., Wagner, L., Wahlestedt, C., Wang, Y., Watanabe, Y., Walls, C., Wilming, L.G., Wynshaw Boris, A., Yanagisawa, M., Yang, I., Yang, L., Yan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P., Hayeteu, N., Hirozane-Kishikawa, T., Konno, H., Nakamura, M., Arakawa, T., Fukuda, S., Hara, A., Hashizuw, M., Imotani, K., Ishi, Y., Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K., Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S., Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNas
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Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S.,
Hirozani,T., Inotani,K., Ishii,Y., Itoh,M., Kawai,J., Konno,H.,
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encyclopedia: real-time sequence clustering for construction of a
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cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Division of Experimental Animal Research in Riken contributed to
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The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9226
Fax: 81-45-503-9216
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/clone_lib="RIKEN full-length enriched, 11 days pregnant
adult female placenta"
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Please visit our web site (http://genome.gsc.riken.go.jp) for
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/clone="1530017M08"
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/strain="C57BL/6J"
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The Institute of Physical and Chemical Research (Kitkh)

1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan rel: 81-45-503-9222

Fax: 81-45-503-9222

Email: genome-ree@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S.,
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Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in Riken
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|-clone="1730037C19"
| cell line="CRL-1722 L5178Y-R"
| cell line="RIKEN full-length enriched, CRL-1722 L5178Y-R"
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Please visit our web site (http://genome.gsc.riken.go.jp) for
further details.
The Institute of Physical and Chemical Research (RIKEN)
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Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S.,
Nikaido,T., Osato,N., Saito,R., Suzuki,H., Yamanaka,I.,
Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A.,
Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C.,
Hume,D.A., Quackehbush,J., Schrimi,L.M., Kanapin,A., Matsuda,H.,
Batalov,S., Beisel,K.W., Blake,J.A., Bradt,D., Brusic,V.,
Fletcher,C.F., Forrest,A., Frazer,K.S., Gaasterland,T.,
Gariboldi,M., Gissi,C., Godzik,A., Gough,J., Grimmond,S.,
Gustinoich,S., Hirokawa,N., Jackson,I.J., Jarvis,B.D., Kanai,A.,
Kawaji,H., Kawasawa,Y., Kediterski,R.M., King,B.L., Konagaya,A.,
Kurochkin,I.V., Lee,Y., Lenhard,B., Lyons,P.A., Maglott,D.R.,
Maltais,L., Marchionni,L., McKenzie,L., Miki,H., Nagashima,T.,
Numata,K., Okido,T., Pevan,W.J., Pertea,G., Pesole,G.,
Ravasi,T., Caroni,L., Reed,D.J., Raid,J., Ring,B.Z., Ringwald,M.,
Sultana,R., Takenaka,Y., Taylor,M., Satou,M., Shimada,K.,
Sultana,R., Takenaka,Y., Taylor,M., Satou,M., Shimada,K.,
Verardo,R., Wagner,L., Wahlestedt,C., Wang,Y., Warenabe,Y.,
Wells,C., Wilming,L.G., Wynshaw-Boris,A., Yanagisawa,M., Yang,I.,
Yang,L., Yang,Z., Zavolan,M., Zhu,Y., Zimmer,A., Carninci,P.,
Hayatsu,N., Hirozane-Kishikawa,T., Yangra,Y., Kawai,J., Alzawa,K.,
Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Alzawa,K.,
Shinagawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander,E.S.,
Rogers,J., Bliraey,B. and Hayashizaki,Y.
Rogers,J., Bliraey,B. and Hayashizaki,Y.
Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNas
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                                                                                                                                                                                               73 CGCTTTGAAGTTAAAAAGTGGAATGCAGTGGCCCTCTGGGCCCTGGGACCATTGTGGTTGAT 132
                                                                                                                                                                                                                                                                                                                          133 AACTGIGCCATCTGCAGCAACCACATTATGGATCTTTGTATCGAATGTCAGGCCAACCAG 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     193 GCGTCAGCTACTTCCGAAGAGTGTACGGTTGCATGGGGAGTCTGCAACCATGCTTTTCAT 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | PheHisCys11eSerArgTrpLeuLysThrArgGlnValCysProLeuAspAsnArgGlu 100
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Sciurognathi, Muridae, Murinae, Mus.
                                   20
                                                                13 ATGGCGGCGATGGATGTGGATACCCCCAGCGGCACCAACAGCGGCGCGGCGAAGAAG 72
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                                                                                                                                                                                                                                                                                   41 AsnCysAlaIleCysArgAsnHisIleMetAspLeuCysIleGluCysGlnAlaAsnGln 60
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                                   MetalaalaalaMetaspValaspThrProSerGlyThrAsnSerGlyAlaGlyLysLys
                                                                                                                                                                                                                                                                                                                                                                                                           61 AlaSerAlaThrSerGluGluCysThrValAlaTrpGlyValCysAsnHisAlaPheHis
                                                                                                                                                           21 ArgPheGluValLysLysTrpAsnAlaValAlaLeuTrpAlaTrpAspIleValValAsp
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Mammalia; Eutheria; Rodentia;
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                                                                                                                                                                                                                                                                                                                                                                           Numacial Butheria; Rodentia; Sciurognath; Muridae; Muscialia Butheria; Rodentia; Sciurognath; Muridae; Muscialia I (Dases I to 362)

1 (Dases I to 362)

8 (Massea II. P. 362)

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Hirozani,K., Ishii,Y., Itoh,M., Kawai,J., Konno,H.,
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Normalization and subtraction of cap-trapper-selected cDNAs to
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prepare full-length cDNA libraries for trapper selected cDNAs to
prepare full-length cDNA libraries for trapper selected conne Res.
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer. Genome Res.
10 (11), 175-1771 (2000)
Computer-based methods for the mouse full-length cDNA
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nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
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Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suchiro-cho, Teurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
                                                                                                               BY099338 RIKEN full-length enriched, pooled tissues, adult spleen, etc. Mus musculus cDNA clone K630127815 5', mRNA sequence.
                                                                              linear
                                                                                  mRNA
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Genomic Sciences Center and Genome Science Laboratory in RIKEN Division of Experimental Animal Research in Riken contributed t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MetAlaAlaAlaMetAspValAspThrProSerGlyThrAsnSerGlyAlaGlyLysLys
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                                                                                  prepare mouse tissues.
Please visit our web site (http://genome.gsc.riken.go.jp)
further details.
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/mol_type="mRNA"
/db_xref="taxon:10090"
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                                                                                                                                                                                                                                                    source
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/mol_type="mRNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (house mouse)
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                                                                                                                                                          Mammaliar, Eucheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. Mammalia; Eucheria; Rodentia; Sciurognathi; Muridae; Mus. 1 (bases 1 to 36)

Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S., Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A., Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C., Hume,D.A., Ouackenbush,J.S., Schriml,L.M., Kanapin,A., Matsuda,H., Batalov,S., Beisel,K.W., Blake,J.A., Bradt,D., Brusic,V., Chothia,C., Corbani,L.B., Cousins,S., Dalla,B., Dragani,T.A., Fletcher,C.F., Graiter,A., Frazer,K.S., Gaarterland,T., Gariboldi,M., Gissi,C., Godzik,A., Gough,J., Grimmond,S., Gustincich,S., Hirokawa,N., Jackson,I.J., Jarvis,B.D., Kanasaya,Y., Kedierski,R.M., King,B.L., Konagaya,A., Kawaji,H., Kawasawa,Y., Kedierski,P.M., King,B.L., Konagaya,A., Kawaji,H., Kawasawa,Y., Lehard,B., Dikt,H., Nagashima,T., Namata,K., Okido,T., Pertea,G., Pertea,G., Pestole,G., Ravasi,T., Reed,J.C., Red,D.J., Reid,J., Ring,B.Z., Ringwald,M., Sandelin,A., Schneider,C., Semple,C.A., Setou,M., Shimada,K., Sultana,R., Takenaka,Y., Taylor,M.S., Tasadale,R.D., Tomita,M., Verardo,R., Walming,L.G., Wynshaw-Boris,A., Yanagisawa,M., Yang,I., Yang,L., Wang,Y., Watenabe,Y., Hayatsu,M., Hirozane-Kishikawa,T., Konno,H., Nakamura,M., Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Alzawa,K., Shinagawa,A., Yasunishi,A., Soshino,M., Waterston,R., Indetail, M., Sato,K., Shiraki,T., Waki,K., Kawai,J., Alzawa,K., Shinagawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander,E.S., Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNas
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Contract: Younged Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute

Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)

1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan

Tel: 81-45-503-9216

Email: genome-resegescriken.jp, URL:http://genome.gsc.riken.jp/
Alzawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S.,
Hirozane,T.: Imotani,K., Ishii,Y., Itoh,M., Kawai,J., Konno,H.,
Miyazaki,A., Murata,M., Nakamura,M., Nomura,K., Numazaki,R.,
Ohno,M., Sakai,K., Sakazume,N., Sasaki,D., Sato,K., Shibata,
Shiraki,T., Tagami,M., Naki,K., Watahiki,A., Muramatsu,M. and
Hayashizaki,Y. Direct Submission
Computational Analysis of Full-Length Mouse cDNAs Compared
Human Genome Sequence Namm. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to
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Computer-based methods for the mouse full-length cDNA
encyclopedia: real-time sequence clustering for construction of a
nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)

CONDUCET-Based methods for the mouse full-length cDNA
encyclopedia: real-time sequence clustering for construction of a
nonredundant cDNA library. Genome Exploration Research Group in Riken
Broyelopedia Project of Genome Exploration Research Group in Riken
Broyelopedia Project of Genome Exploration Research Group in Riken
Davision of Experimental Animal Research in Riken contributed to
                                                                                                            Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus.
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Please visit our web site (http://genome.gsc.riken.go.jp) for
further details.
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                                                                                                            Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                             musculus (house mouse)
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TITLE

COMMENT

/organism="Mus musculus"

Location/Qualifiers

source

FEATURES

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 362)

Stati, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Nikaido, I., Osato, N., Saito, R., Suzuki, H., Yamanaka, I., Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Mogami, A., Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Mogami, A., Kiyosawa, H., Mogami, T., Hume, D. A., Quackenbush, J., Schriml, L. M., Kanapii, A., Matsuda, H., Batalov, S., Beisel, K.W., Blake, J.A., Bradt, D., Brusic, V., Chothia, C., Corbani, L. E., Cousins, S., Dalla, E., Dragani, T. A., Fletcher, C.F., Forrest, A., Frazer, K.S., Gasterland, T., Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S., Gustinoich, S., Hirokawa, N., Jackson, I.J., Jarvis, E.D., Kanai, A., Kurochkin, I. V., Lee, Y., Lenhard, B., Lyons, P.A., Maglott, D.R., Nuata, K., Okido, T., Pervan, M., Petres, G., Pesole, G., Petrovsky, N., Pillai, R., Pontius, J.O., Petrovsky, N., Pillai, R., Pontius, J.O., Ranachandran, S., Ravasi, T., Reed, J.C., Reed, D.J., Reid, J., Ring, B.Z., Ringwald, M.,
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Matches:
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Mismatches:
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80 decrirgaagriaaaagresaarecagrescerteresecereseareriseresingi 139
      20 ATGGCGGCGGTGGATGTGGATACCCCCAGCGGCACCAACAACAGCGGCGCGCGAAGAAG 79
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Sandelin, A., Schneider, C., Semple, C.A., Setou, M., Shimada, K., Takenaka, Y., Taylor, M.S., Teasdale, R.D., Tomita, M., Verardo, R., Wadner, L., Wahlested, C., Wang, Y., Watanabe, Y., Welle, C., Wilming, L.G., Wynhaw-Boris, A., Yanagiawa, M., Yang, I., Yang, L., Yuan, Z. Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P., Hayatsu, N., Hirozane-Kishikawa, T., Komuo, H., Nakamura, M., Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K., Sakazume, N., Kawai, J., Aizawa, K., Itoh, M., Kagwa, I., Miyazaki, T., Waki, K., Sasaki, D., Shibata, K., Shinagawa, I., Yoshino, M., Waterston, R., Lander, E.S., Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: genome-reseggc.riken.jp, URL:http://genome.gsc.riken.jp/
Alzawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S.,
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encyclopedia: real-time sequence clustering for construction of a
nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
CDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      prepare mouse tissues.
Tissues were provided by Vassilis Aidinis ( Biomedical Sciences
Research Center 'Al. Fleming' Institute of Immunology 14-16 Al.
Fleming street 16672 Vari, Greece ) whose assistance we gratefully
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          visit our web site (http://genome.gsc.riken.go.jp) for
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/clone_lib="RIKEN full-length enriched, whole joints"

    .362
    /organism="Mus musculus"

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Mus musculus (nouse mouse)

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 364)

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Butalov, S. (Beisel, K. W. Blake, J. M. Erade, D. , Brusic, V. (Corbani, L. B. ) (Corbani, L. ) (Corbani, L. B. ) (Corbani, L. Barde, D. ) (Corbani, L. B. ) (Corbani, L. ) 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BY036231 RIKEN full-length enriched, 14 days pregnant adult female amnion Mus musculus CDNA clone I530023F07 5', mRNA sequence.
                                                                                                                          140 AACTGTGCCATCTGCAGGAACCACATTATGGATCTTTGTATCGAATGTCAGGCCAACCAG 199
                                                                                                                                                                                                                                                                                                                                                                 260 TTCCACTGCATCTCTCGATGGCTCAAAACGAGGCAGGTGTGTCCGTTGGACAACAGAGAG 319
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The Institute of Physics Of Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
                                                                                                                                                                                                                                                                                                                  81 PheHisCysIleSerArgTrpLeuLysThrArgGlnValCysProLeuAspAsnArgGlu 100
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Length: Matches: Conservative: Mismatches: Indels:

9.19e-61 616.00 100.00% 100.00%

Percent Similarity: Best Local Similarity:

Pred. No.:

Query Match: DB:

Gaps:

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322 TGGGAGTTCCAGAAGTATGGGCAT 345
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Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S.,
Hirozand,K., Ishii,Y., Tichl,M., Kawai,J., Konno,H.,
Miyazaki,A., Murata,M., Nakamura,M., Nomura,K., Numazaki,R.,
Ohno,M., Sakai,K., Sakazume,M., Namura,K., Numazaki,R.,
Shiraki,T., Tagami,M., Naki,K., Watahiki,A., Muramatsu,M. and
Hayashizaki,Y. Direct Submission Compute converse of the Aragami, M., Waki,K., Watahiki,A., Muramatsu,M. and
Hayashizaki,Y. Direct Submission Conpute converse of the Computational Analysis of Full-Length Mouse cDNAs Computerional Analysis of Full-Length Mouse cDNAs Compared with
Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
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RIKEN integrated sequence analysis (RISA) system-384-format
sequencing pipeline with 384 multicapillary sequencer. Genome Res.
10 (11), 175-1771 (2000)
Computer-based methods for the mouse full-length cDNA
encyclopedia: real-time sequence clustering for construction of a
nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
CONDUCE-based methods for the mouse Eull-length cDNA
encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Exploration Research Group in Riken
proporare mouse finance and Animal Research in Riken contributed to
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Please visit our web site (http://genome.gsc.riken.go.jp) for
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adult Female amnion"
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Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
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Okazaki, Y. Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Nikaido, I., Osato, N., Saito, R., Suzuki, H., Yamanaka, I., Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D. P., Bult, C., Hume, D.A., Quackenbush, J., Schriml, L. M., Kanapin, A., Matsuda, H., Batalov, S., Belsel, K., W., Blake, J. A., Bradt, D., Brusic, V., Chothia, C., Corbani, L. E., Cousins, S., Dalla, E., Dragani, T. A.,
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                                                                                                                                        1. .364
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/clone="K630081M12"
/clone="K630081M12"
/clone labe awhole body"
/clone labe RIXEN full-length enriched, 14 days embryowhole body"
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                                                          prepare mouse tissues.
Please visit our web site (http://genome.gsc.riken.go.jp) for
further details.
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Fletcher, C.F., Forrest, A., Frazer, K.S., Gaasterland, T., Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Garimond, S., Gustinoch, S., Hirokawa, N., Jackson, I.J., Javis, B.D., Kanai, A., Kawasaya, Y., Kediareshi, R.M., King, B.L., Konagaya, A., Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Maglott, D.R., Maltais, L., Marchinonni, L., McKenzie, L., Miki, H., Nagashima, T., Numata, K., Okido, T., Pavan, W.J., Pertea, G., Pesole, G., Petrovsky, N., Pillai, R., Pontius, J.U., Qi, D., Ramachardran, S., Ravasi, T., Reed, J.C., Semple, C.A., Setou, M., Shingwald, M., Sandelin, A., Schneider, C., Semple, C.A., Teasdale, R.D., Tomita, M., Verardo, R., Wagner, Y., Taylor, M.S., Teasdale, R.D., Tomita, M., Wells, C., Willming, L.G., Wynshaw-Boris, A., Yanagaswa, Y., Yang, I., Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Garninci, P., Hayatsu, N., Hirozane-Kishikawa, T., Konno, H., Nakamura, M., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K., Arawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Satowa, J., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K., Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S., Rogers, J., Birney, E. and Hayashizaki, Y. Rogers, J., Birney, E. and Hayashizaki, Y. Rogers, J., Birney, E. and Hayashizaki, Y. Mature, 420, 563-573 (2002)
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Email: genome-ree@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S.,
Hirozante,T., Imotani,W., Ishii,Y., Itoh,M., Kawai,J., Konno,H.,
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Ohno,M., Sakai,K., Sakazume,M., Sasaki,D., Sato,K., Shibata,K.,
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Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer. Genome Res.
10 (11), 1757-1771 (2000)
Computer-based methods for the mouse full-length cDNA
encyclopedia: real-time sequence clustering for construction of a
nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
CDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
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Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
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clone lib="RIKEN full-length enriched, 15 days pregnant
adult Female amnion"
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Please visit our web site (http://genome.gsc.riken.go.jp) for
further details.
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/clone="K630136007"
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/strain="C57BL/6J"
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Contact: Yoshinde Hayashizaki.
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Ephysical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9216
Fax: 81-45-503-9216
Fax: 81-45-503-9216
Faxishiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9216
Faxishiro-cho, Mimura, T., Arakawa, T., Carninci, P., Fukuda, S., Hirozanne, T., Imotani, K., Ishii, Y., Itoh, M., Kawai, J., Konno, H., Miyazaki, A., Murata, M., Nakamura, M., Nomura, K., Numazaki, R., Ohno, M., Sakai, K., Sakaume, N., Sasaki, D., Sato, K., Shibata, K., Shizaki, T. Tagami, M., Waki, K., Watahiki, A., Muramatsu, M. and Hayashizaki, Y. Direct Submission Computer Computer Sequences Mamm. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected CDMAs to prepare full-length cDMA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a norredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
CDNA library was prepared and sequence din Muse Genome Encyclopedia Project of Genome Exploration Research Group Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tissues were provided by Michela Fagiolini and Takao K. Hensch (
Laboratory for Neuronal Circuit Development Brain Science Institute
RIKEN 2-1 Hirosawa, Wakk-shi, Saitama 351-0198 Japan ) Whose
assistance we gratefully acknowledge. Please visit our web site
(http://genome.gsc.riken.go.jp) for further details.
Location/Qualifiers
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/mol_type="mRNA"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="K530330G11"
/tissue type="wisual cortex"
/clone_lib="RIKEN full-length enriched, visual cortex"
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                                                                                                                               Contact: Yoshihide Hayashizaki
                              Nature 420, 563-573 (2002)
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ENKARYOCAS, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Nammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1. (bases 1 to 370)

8. (kazaki, Y.; Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Nikaido, I., Osato, N., Saito, R., Suzuki, H., Yamanaka, I., Kayosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D.P., Bult, C., Golobori, T., Baldarelli, R., Hill, D.P., Bult, C., Corbani, L.E., Cousins, S., Bradic, V., Brusic, V., Chothia, C., Corbani, L.E., Cousins, S., Dalla, E., Dragani, T.A., Fletcher, C.F., Forrest, A., Frazer, K.S., Gaasterland, T., Garimold, M., Gissi, C., Godik, A., Gough, J., Grimmond, S., Garibodi, M., Gissi, C., Godik, A., Gough, J., Grimmond, S., Kawaji, H., Kawasawa, Y., Kedzlerski, R.M., King, B.L., Konagaya, A., Kawail, H., Kawasawa, Y., Kedzlerski, R.M., King, B.L., Marchioni, I., McKenzie, L., Marvis, P.A., Maglott, D.R., Marchioni, I., McKenzie, J., Miki, H., Nagashima, T., Numata, K., Okido, T., Pevan, W.J., Pertea, G., Pesole, G., Fetroveky, N., Pillai, R., Pontius, J.U., Gi, D., Ramachandran, S., Ravasi, T., Reed, J.C., Reed, D.J., Ring, Y., Sandelin, A., Schneider, C., Semple, C.A., Setou, M., Shimada, K., Vang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P., Vang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P., Vang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P., Kawa, T., Koma, J., Matanaba, I., Mirozane, R., Sakai, K., Sakai, D., Aizawa, K., Shiraki, T., Washer, T., Komon, M., Materaton, R., Shibata, Y., Shiraki, T., Washer, Y., Sakai, K., Sakai, K., Sakai, K., Sakai, K., Sakai, Y., Sakai, Y., Sakai, Y., Sakai, Y., Shiraki, Y., Sakai, Y., Sakai, Y., Sakai, Y., Sakai, Y., Shiraki, Y., Shiraki, Y., Sakai, Y.
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BY294825 RIKEN full-length enriched, visual cortex Mus musculus
CDNA clone K530330G11 5', mRNA sequence.
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Mus musculus
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Mus musculus (house mouse)
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                                                                                                                                                                                                                                                                                                                                                                                           BY320216 BY320216 RIKEN full-length enriched, osteoclast-like cell Mus musculus cDNA clone I420104MI7 5', mRNA sequence.
                                                                                    Contact: Yoshihide Hayashizaki
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Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
T-722 Suchiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
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Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S.,
Hirozane,T., Imotani,K., Ishii,Y., Itoh,M., Kwai,J., Konno,H.,
Miyazaki,A., Murata,M., Nakamura,M., Nomura,K., Numazaki,R.,
Ohno,M., Sakai,K., Sakazume,N., Saeaki,D., Sato,K., Shibata,K.,
Shiraki,T., Tagami,M., Waki,K., Watahiki,A., Muramatsu,M. and
Hayashizaki,Y. Direct Submission
Computational Analysis of Full-Length Mouse CDNAs Compared with
Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to
210 GCGTCAGCTACTTCCGAAGAGTGTACGTTGCATGGGGGAGTTGTGCAACCATGCTTTTCAT
                                                                                                                                                                                                               101 TrpGluPheGlnLysTyrGlyHis 108
                                                                                                                                                                                                                                                 330 TGGGAGTTCCAGAAGTATGGGCAT 353
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BY320216.1 GI:26510553
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TITLE

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prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)

RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)

Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
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                                                                                                                                                                                                                                                                                                                                                              Tissues were provided by Takashi Ishikawa ( Department of Surgery 2 Yokohama City University 3-9 Fukuura,Kanazawa-ku,Yokohama 236-0004 Japan ) whose assistance we gratefully acknowledge. Please visit our web site (http://genome.gsc.riken.go.jp) for further details.

Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  90 GCTTTGAAGTTAAAAAGTGGAATGCAGTGGCCCTCTGGGCCTGGGACATTGTGGTTGAT 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           209
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /cell_type="osteoclast-like cell"
/clone_lib="RIKEN full-length enriched, osteoclast-like
cell"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          150 AACTGTGCCATCTGCAGGAACCACTTATGGATCTTTGTATCGAATGTCAGGCCAACCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   41 AsnCysAlaIleCysArgAsnHisIleMetAspLeuCysIleGluCysGlnAlaAsnGln
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    210 GCGTCAGCTACTTCCGAAGAGTGTACGGTTGCATGGGGAGTCTGCAACCATGTTCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21 ArgPheGluValLysLysTrpAsnAlaValAlaLeuTrpAlaTrpAspIleValValAsp
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108
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0
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Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /db xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-541-462B-2 (1-108) x BY320216 (1-371)
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616.00
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100.00%
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ORGANISM

REFERENCE AUTHORS

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Musucitus Butheria; Rodentia; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. E. (Dasses I to 374)

E. (Dasses I, D. 374)

Nikaido, I., Osato, N., Saito, R., Suzuki, H., Yamanaka, I., Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D. P., Bult, C., Hume, D. A., Quackenbush, J., Schriml, L. M., Kanapin, A., Matsuda, H., Batalory, S., Bassel, K. W., Blake, J. A., Dalla, E., Dragani, T. A., Pletcher, C. R., Forrest, A., Frazer, K.S., Gaasterland, T., Corbani, L. E., Cousins, S., Dalla, E., Dragani, T. A., Pletcher, C. R., Forrest, A., Frazer, K.S., Gaasterland, T., Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Jarvis, E. D., Konagaya, A., Kawasawa, Y., Redzierski, R. M., King, B. L., Konagaya, A., Kawaji, H., Kawasawa, Y., Edzierski, R. M., King, B. L., Konagaya, A., Karochkin, I. V., Lee, Y., Lenhard, B., Lyons, P. M., Maglott, D. R., Matchionni, L., McKenzie, L., Miki, H., Nagashima, T., Numata, K., Okido, T., Pavan, W.J., Pertea, G., Pesole, G., Petread, J.C., Reed, J.C., Reed, J.C., Reid, J., Ring, B. Z., Ringwald, M., Sandelin, A., Schneider, C., Semple, C. A., Setou, M., Shimada, K., Sulteana, R., Takenaka, Y., Taylor, M.S., Teasdale, R.D., Tomita, M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone="1920043008"
/tissue_type="kidney"
/dev_stage="17 days embryo"
/clone_lib="RIKEN full-length enriched, 17 days embryo
kidney"
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BY294855 RIKEN full-length enriched, visual cortex Mus musculus cDNA clone K530330K07 5', mRNA sequence.
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_xref="taxon:10090"
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BY294855.1 GI:26485192
EST.
Mus musculus (house mouse)
Mus musculus
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                 Musuciania, Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Musurania; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (Dases 1 to 373)

S. Cazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Nikaido, I., Osato, N., Saito, R., Suzuki, H., Yamanaka, I., Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Mogami, A., Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D.P., Bult, C., Riyosawa, H., Basisel, K., Hasegawa, Y., Mogami, A., Matsuda, H., Batsel, K., Blake, J.A., Bradt, D., Brusic, V., Chothia, C., Corbani, L.E., Cousines, S., Dalla, E., Dragani, T.A., Gissi, C., Godzik, A., Gough, J., Grimmond, S., Gustincich, S., Hirokawa, N., Jackson, I.J., Nardi, E.D., Kanagani, T.A., Kawaji, H., Kawasawa, Y., Kedzierski, R.M., King, B.L., Konagaya, A., Kawaji, H., Kawasawa, Y., Kedzierski, R.M., King, B.L., Konagaya, A., Multais, L., Marchionni, L., Mokenie, L., Miki, H., Nagashima, T., Numata, K., Okido, T., Pavan, W.J., Pertea, G., Pesole, G., Perorokky, N., Pillai, R., Pontius, J.U., Qi, D., Kamachandran, S., Ravasi, T., Reed, J.C., Reed, D.J., Recid, J., Randandran, S., Sandelin, A., Schneider, C., Semple, C.A., Setou, M., Shimada, K., Sultana, R., Takonaka, Y., Taylor, M.S., Tasadale, R.D., Tomata, W., Verardo, R., Wagner, L., Wanlestedt, C., Wang, Y., Watanabe, Y., Wallanabe, Y., Wallanabe, L., Walla, K., Sawa, Y., Kadawa, T., Wansa, K., Sawa, Y., Kadawa, T., Wansa, Y., Carolan, M., Sato, K., Shiraki, T., Wang, Y., Waterston, R., Lander, E.S., Shinagawa, A., Yasunishi, A., Sahai, K., Sasaki, D., Shibata, K., Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S., Analysis of the Mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
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Email: genome-res@gec.riken.jp, URL:http://genome.gec.riken.jp/
Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S.,
Hirozane,T., Imotani,K., Ishii,Y., Itoh,M., Kawai,J., Konno,H.,
Miyazaki,A., Murata,M., Nakamura,M., Nawai,J., Sato,K., Shibata,K.,
Shiraki,T., Tagami,M., Waki,K., Watahiki,A., Muramatsu,M. and
Hayashizaki,Y. Direct Submission
Computational Analysis of Full-Length Mouse cDNAs Compared
Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected CDNAs to
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RIKEN integrated sequence analysis (RISA) system--384-format
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10 (11), 1757-1771 (2000)
Computer-based methods for the mouse full-length cDNA
encyclopedia: real-time sequence clustering for construction of a
nonredundant cDNA library Genome Res. 11 (2), 281-289 (2001)
CDNA library was prepared and sequence Laboratory in Riken
Genomic Sciences Center and Genome Exploration Research Group in Riken
Division of Experimental Animal Research in Riken contributed to
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Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
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BY037694 BIKEN full-length enriched, CRL-1722 L5178Y-R Mus musculus CDNA clone I730002F15 5', mRNA sequence.
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Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S.,
Hirozane,T., Imctani,K., Ishli,Y., Itoh,M., Kawai,J., Konno,H.,
Miyazaki,A., Murata,M., Nakamura,M., Nomura,K., Numazaki,R.,
Ohno,M., Sakai,K., Sakazume,N., Sasaki,D., Sato,K., Shizata,R.,
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Verardo, R., Wagner, L., Wahlestedt, C., Wang, Y., Watanabe, Y., Walls, C., Wilming, L.G., Wynshaw-Boris, A., Yanagisawa, M., Yang, I., Yang, L., Yanan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P., Savolan, M., Zhu, Y., Zimmer, A., Carninci, P., Sakazume, N., Sato, K., Shiraki, T., Konno, H., Nakamura, M., Indrawa, T., Kukuda, K., Hara, A., Hashizume, W., Imotani, K., Ishii, Y., Arakwa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii, Y., Shinagawa, A., Yasunishi, A., Sakai, K., Sasaki, D., Shibata, K., Rogers, J., Birney, E. and Hayashizaki, Y. Analysis of the mouse transcriptome based on functional annotation of 60, 770 full-length colbas
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                                                                                                                                                                                                                                                                                                                                                                                                          Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken. Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             prepare mouse tissues. Tissues were provided by Michela Fagiolini and Takao K. Hensch (
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Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Fax: 81-45-503-9216
                                                                                                                                                                                                                                                                                                                                        Rogers, J., Birney, E. and Hayashizaki, Y. Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Yoshihide Hayashizaki
Mus musculus (house mouse)
Mus musculus
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Sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
Computer-based methods for the mouse full-length cDNA computer-based methods for the mouse full-length cDNA computer-based methods sequence clustering for construction of a nonredundant cDNA library Genome Res. 11 (2), 281-289 (2001) cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

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